FIG.1A

```
                   148       178       208       238       268       298
FRI-1              ALLVFLDIIEWTTQETFPPKYLHYDPETGRQLLCDKCAPGTYLKQHCTVRRKTLCVPCPD
                                               |:  | ||:||    |  ||    |:| :| |
SW:TNR2_HUMAN      HALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCED
                          30        40        50        60        70        80

                   328
FRI-1              YSYTDSWHTS
                    :||: |:
SW:TNR2_HUMAN      STYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPL
                          90       100       110       120       130       140
```

FIG.1B

```
FRI-1          69 YLHYDPETGRQLLCDKCAPGTYLKQHC.TVRRKTLCV.PCPDY.SYTDSW
                  |  |.  ...   | .| || :|  .|     :  |  |   || :    |.| .
TNFR profile    6 YHYYDQNGRMCEECHMCQPGHFLVKHCKQPKRDTVCHKPCEPGVTYTDDW

FRI-1         116 H
                  |
TNFR profile   56 H
```

Z Score = 8.29

FIG. IC

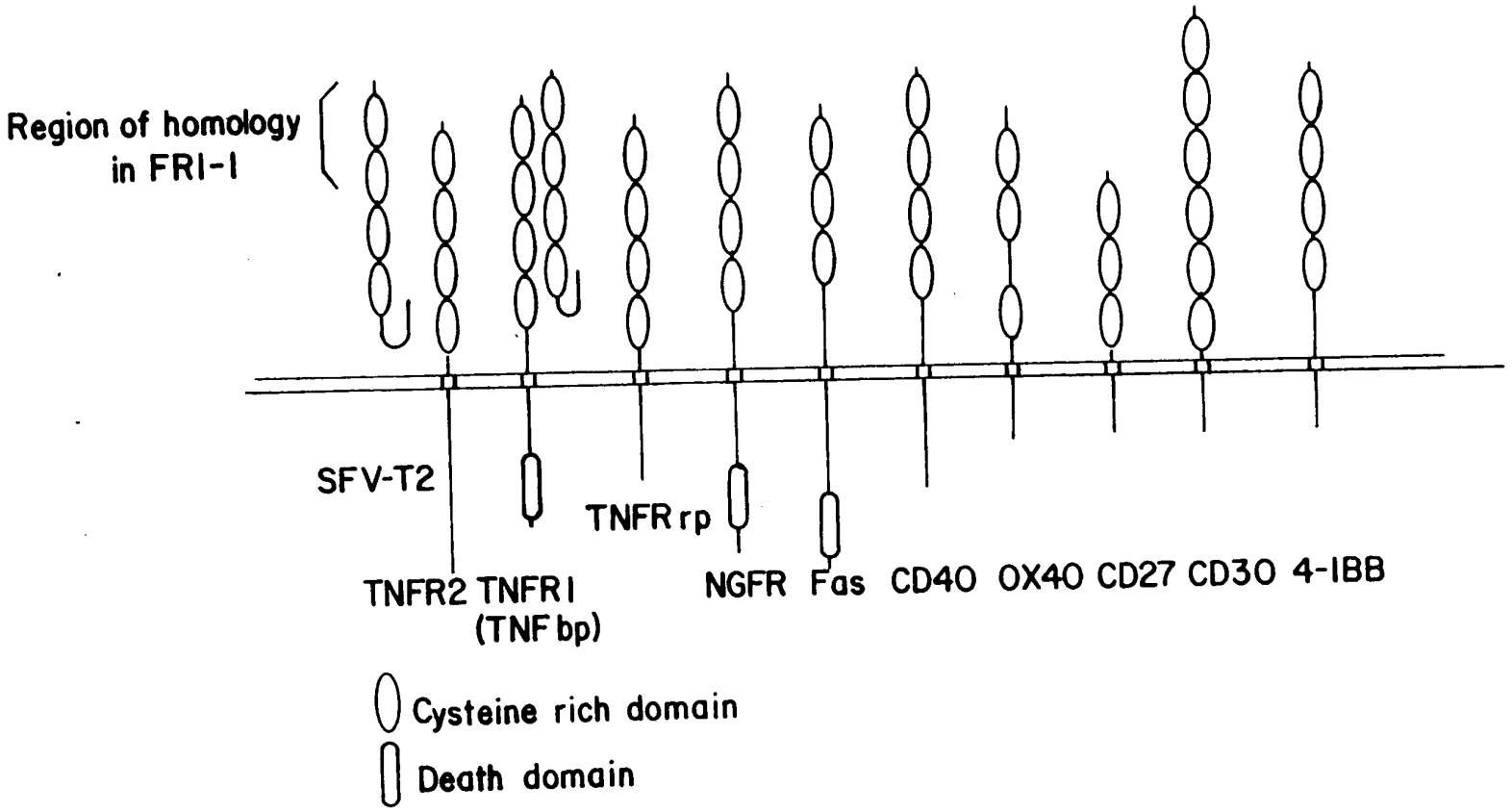


FIG.2A

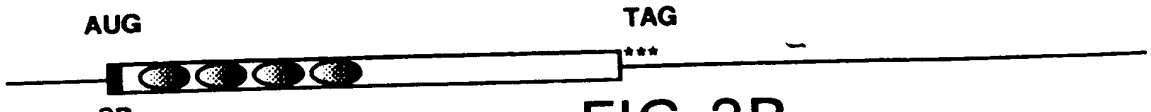


FIG.2B

```
          10                  30                  50
ATCAAAGGCAGGGCATACTTCCTGTTGCCCAGACCTTATATAAAACGTCATGTTCGCCTG
          70                  90                 110
GGCAGCAGAGAAGCACCTAGCACTGGCCCAGCGGCTGCCGCCTGAGGTTTCCAGAGGACC
         130                 150                 170
ACAATGAACAAGTGGCTGTGCTGTGCACTCCTGGTGTTCTTGGACATCATTGAATGGACA
   M   N   K   W   L   C   C   A   L   L   V   F   L   D   I   I   E   W   T
         190                 210                 230
ACCCAGGAAACCTTTCCTCCAAAATACTTGCATTATGACCCAGAAACCGGACGTCAGCTC
T   Q   E   T   F   P   P   K   Y   L   H   Y   D   P   E   T   G   R   Q   L
         250                 270                 290
TTGTGTGACAAATGTGCTCCTGGCACCTACCTAAAACAGCACTGCACAGTCAGGAGGAAG
L   C   D   K   C   A   P   G   T   Y   L   K   Q   H   C   T   V   R   R   K
         310                 330                 350
ACACTGTGTGTCCCTTGCCCTGACTACTCTTATACAGACAGCTGGCACACGAGTGATGAA
T   L   C   V   P   C   P   D   Y   S   Y   T   D   S   W   H   T   S   D   E
         370                 390                 410
TGCGTGTACTGCAGCCCCGTGTGCAAGGAACTGCAGACCGTGAAACAGGAGTGCAACCGC
C   V   Y   C   S   P   V   C   K   E   L   Q   T   V   K   Q   E   C   N   R
         430                 450                 470
ACCCACAACCGAGTGTGCGAATGTGAGGAAGGGCGCTACCTGGAGCTCGAATTCTGCTTG
T   H   N   R   V   C   E   C   E   E   G   R   Y   L   E   L   E   F   C   L
         490                 510                 530
AAGCACCGGAGCTGTCCCCCAGGCTTGGGTGTGCTGCAGGCTGGGACCCCAGAGCGAAAC
K   H   R   S   C   P   P   G   L   G   V   L   Q   A   G   T   P   E   R   N
         550                 570                 590
ACGGTTTGCAAAAGATGTCCGGATGGGTTCTTCTCAGGTGAGACGTCATCGAAAGCACCC
T   V   C   K   R   C   P   D   G   F   F   S   G   E   T   S   S   K   A   P
         610                 630                 650
TGTAGGAAACACACCAACTGCAGCTCACTTGGCCTCCTGCTAATTCAGAAAGGAAATGCA
C   R   K   H   T   N   C   S   S   L   G   L   L   L   I   Q   K   G   N   A
         670                 690                 710
ACACATGACAATGTATGTTCCGGAAACAGAGAAGCAACTCAAAATTGTGGAATAGATGTC
T   H   D   N   V   C   S   G   N   R   E   A   T   Q   N   C   G   I   D   V
         730                 750                 770
ACCCTGTGCGAAGAGGCATTCTTCAGGTTTGCTGTGCCTACCAAGATTATACCGAATTGG
T   L   C   E   E   A   F   F   R   F   A   V   P   T   K   I   I   P   N   W
         790                 810                 830
CTGAGTGTTCTGGTGGACAGTTTGCCTGGGACCAAAGTGAATGCAGAGAGTGTAGAGAGG
L   S   V   L   V   D   S   L   P   G   T   K   V   N   A   E   S   V   E   R
         850                 870                 890
ATAAAACGGAGACACAGCTCGCAAGAGCAAACTTTCCAGCTACTTAAGCTGTGGAAGCAT
I   K   R   R   H   S   S   Q   E   Q   T   F   Q   L   L   K   L   W   K   H
         910                 930                 950
CAAAACAGAGACCAGGAAATGGTGAAGAAGATCATCCAAGACATTGACCTCTGTGAAAGC
Q   N   R   D   Q   E   M   V   K   K   I   I   Q   D   I   D   L   C   E   S
         970                 990                1010
AGTGTGCAACGGCATATCGGCCACGCGAACCTCACCACAGAGCAGCTCCGCATCTTGATG
S   V   Q   R   H   I   G   H   A   N   L   T   T   E   Q   L   R   I   L   M
```

FIG.2C

```
        1030                                   1050                                   1070
GAGAGCTTGCCTGGGAAGAAGATCAGCCCAGACGAGATTGAGAGAACGAGAAAGACCTGC
E  S  L  P  G  K  K  I  S  P  D  E  I  E  R  T  R  K  T  C
        1090                                   1110                                   1130
AAACCCAGCGAGCAGCTCCTGAAGCTACTGAGCTTGTGGAGGATCAAAAATGGAGACCAA
K  P  S  E  Q  L  L  K  L  L  S  L  W  R  I  K  N  G  D  Q
        1150                                   1170                                   1190
GACACCTTGAAGGGCCTGATGTACGCACTCAAGCACTTGAAAGCATACCACTTTCCCAAA
D  T  L  K  G  L  M  Y  A  L  K  H  L  K  A  Y  H  F  P  K
        1210                                   1230                                   1250
ACCGTCACCCACAGTCTGAGGAAGACCATCAGGTTCTTGCACAGCTTCACCATGTACCGA
T  V  T  H  S  L  R  K  T  I  R  F  L  H  S  F  T  M  Y  R
        1270                                   1290                                   1310
TTGTATCAGAAACTCTTTCTAGAAATGATAGGGAATCAGGTTCAATCAGTGAAGATAAGC
L  Y  Q  K  L  F  L  E  M  I  G  N  Q  V  Q  S  V  K  I  S
        1330                                   1350                                   1370
TGCTTATAGTTAGGAATGGTCACTGGGCTGTTTCTTCAGGATGGGCCAACACTGATGGAG
C  L
        1390                                   1410                                   1430
CAGATGGCTGCTTCTCCGGCTCTTGAAATGGCAGTTGATTCCTTTCTCATCAGTTGGTGG
        1450                                   1470                                   1490
GAATGAAGATCCTCCAGCCCAACACACACACTGGGGAGTCTGAGTCAGGAGAGTGAGGCA
        1510                                   1530                                   1550
GGCTATTTGATAATTGTGCAAAGCTGCCAGGTGTACACCTAGAAAGTCAAGCACCCTGAG
        1570                                   1590                                   1610
AAAGAGGATATTTTTATAACCTCAAACATAGGCCCTTTCCTTCCTCTCCTTATGGATGAG
        1630                                   1650                                   1670
TACTCAGAAGGCTTCTACTATCTTCTGTGTCATCCCTAGATGAAGGCCTCTTTTATTTAT
        1690                                   1710                                   1730
TTTTTTATTCTTTTTTTCGGAGCTGGGGACCGAACCCAGGGCCTTGCGCTTGCGAGGCAA
        1750                                   1770                                   1790
GTGCTCTACCACTGAGCTAAATCTCCAACCCCTGAAGGCCTCTTTCTTTCTGCCTCTGAT
        1810                                   1830                                   1850
AGTCTATGACATTCTTTTTTCTACAATTCGTATCAGGTGCACGAGCCTTATCCCATTTGT
        1870                                   1890                                   1910
AGGTTTCTAGGCAAGTTGACCGTTAGCTATTTTTCCCTCTGAAGATTTGATTCGAGTTGC
        1930                                   1950                                   1970
AGACTTGGCTAGACAAGCAGGGGTAGGTTATGGTAGTTTATTTAACAGACTGCCACCAGG
        1990                                   2010                                   2030
AGTCCAGTGTTTCTTGTTCCTCTGTAGTTGTACCTAAGCTGACTCCAAGTACATTTAGTA
        2050                                   2070                                   2090
TGAAAATAATCAACAAATTTTATTCCTTCTATCAACATTGGCTAGCTTTGTTTCAGGGC
        2110                                   2130                                   2150
ACTAAAAGAAACTACTATATGGAGAAAGAATTGATATTGCCCCCAACGTTCAACAACCCA
        2170                                   2190                                   2210
ATAGTTTATCCAGCTGTCATGCCTGGTTCAGTGTCTACTGACTATGCGCCCTCTTATTAC
        2230                                   2250                                   2270
TGCATGCAGTAATTCAACTGGAAATAGTAATAATAATAATAGAAATAAAATCTAGACTCC
        2290                                   2310                                   2330
ATTGGATCTCTCTGAATATGGGAATATCTAACTTAAGAAGCTTTGAGATTTCAGTTGTGT
        2350                                   2370                                   2390
TAAAGGCTTTTATTAAAAAGCTGATGCTCTTCTGTAAAAGTTACTAATATATCTGTAAGA
        2410                                   2430
CTATTACAGTATTGCTATTTATATCCATCCAG
```

FIG.2D

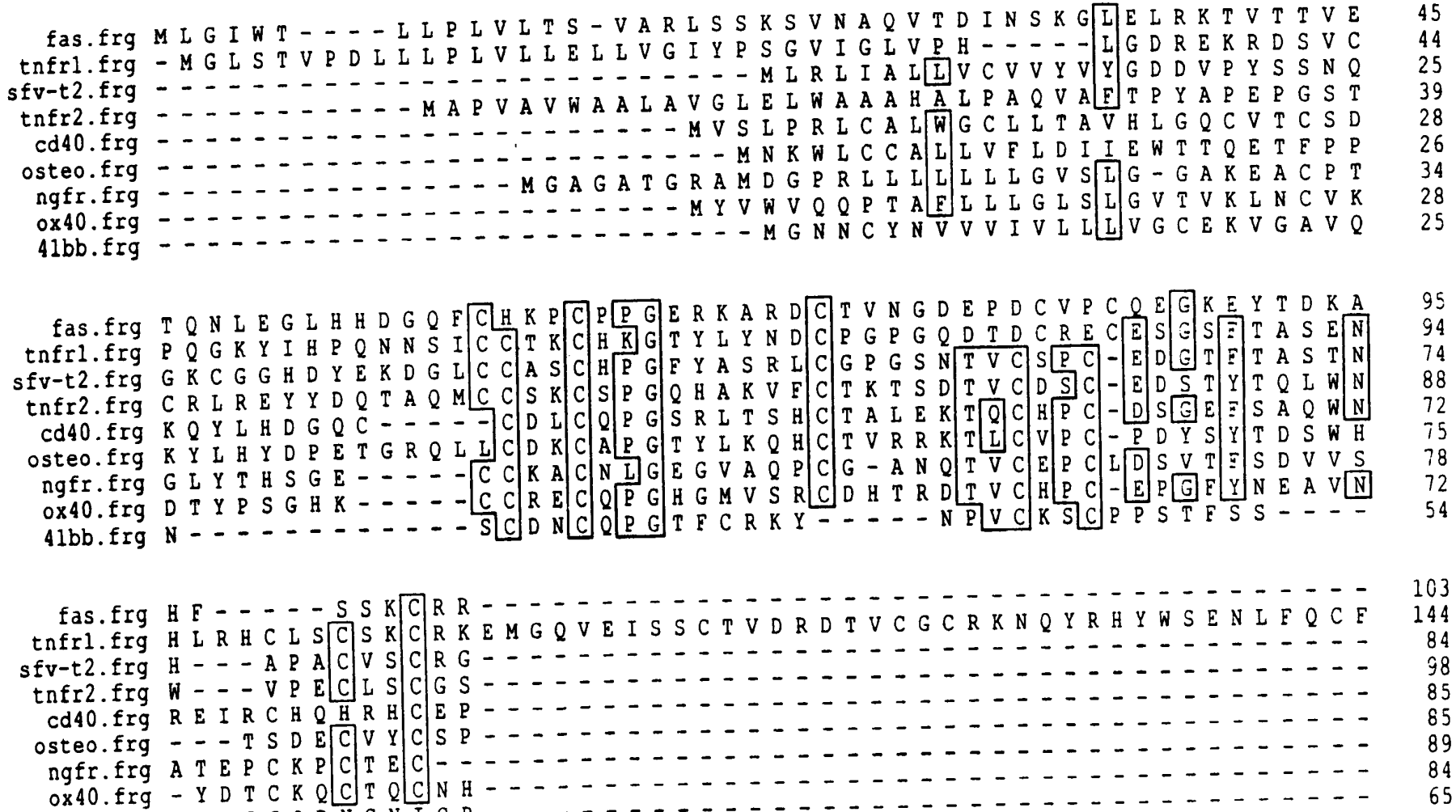


FIG.2E

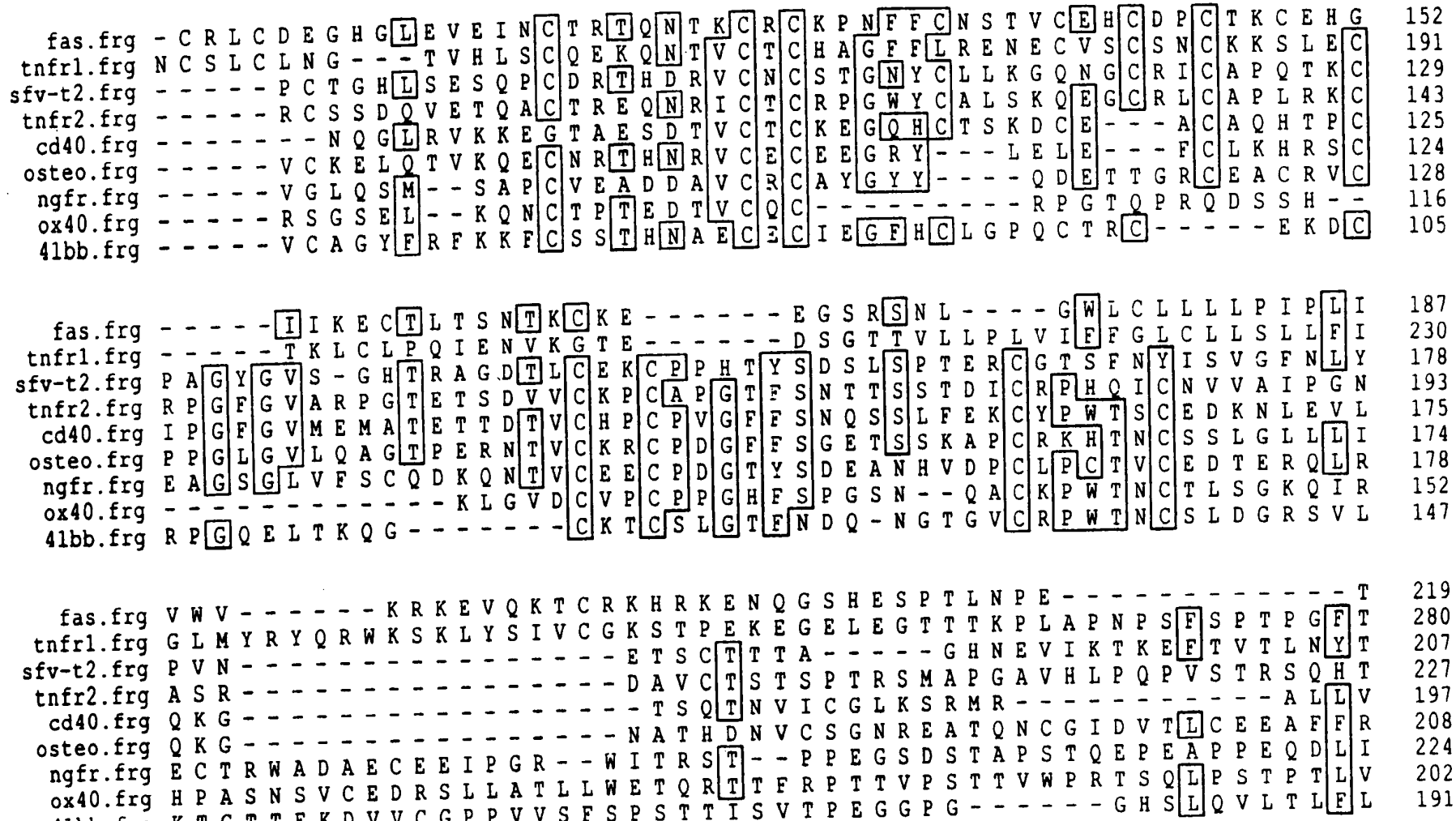


FIG.3A
FIG.3B
FIG.3C
FIG.3D
FIG.3E

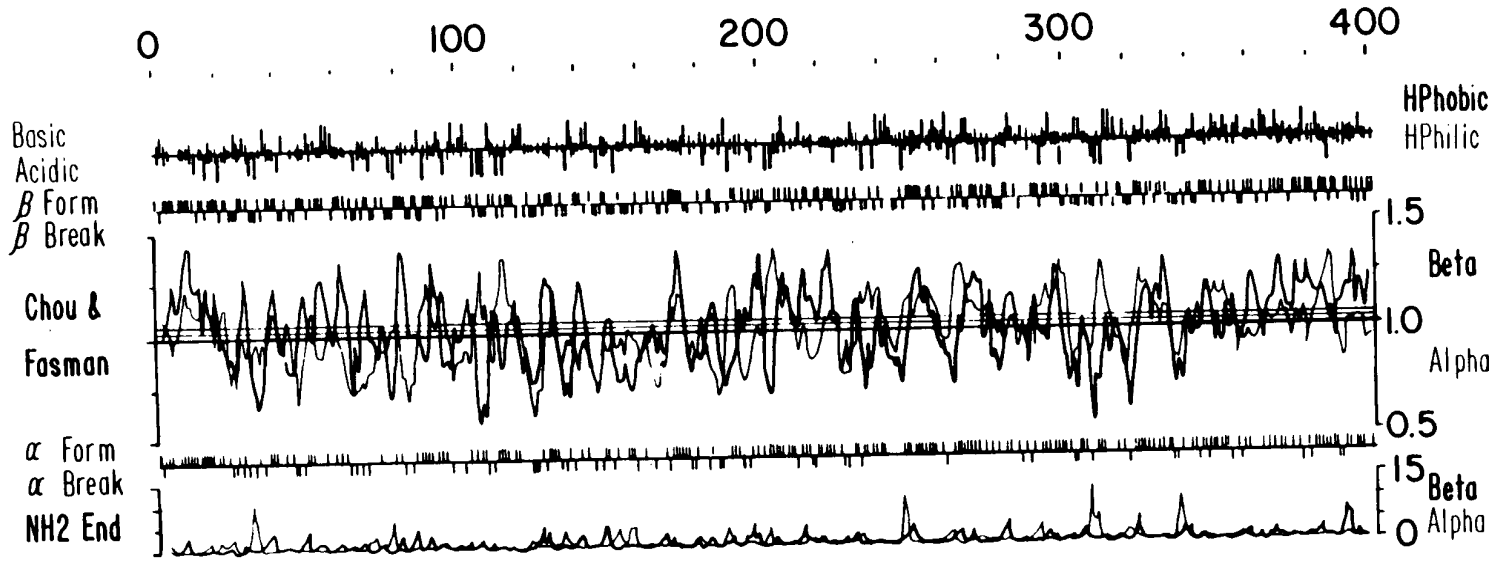


FIG.3F

FIG.3G

FIG.3H

FIG.3I

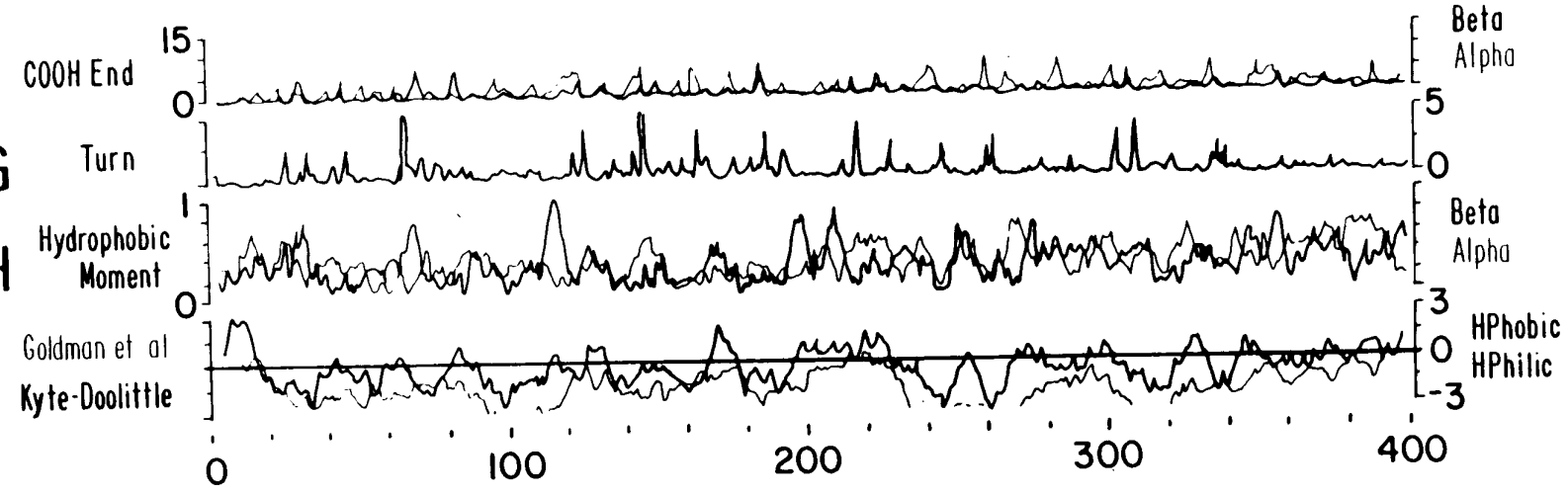


FIG.4A

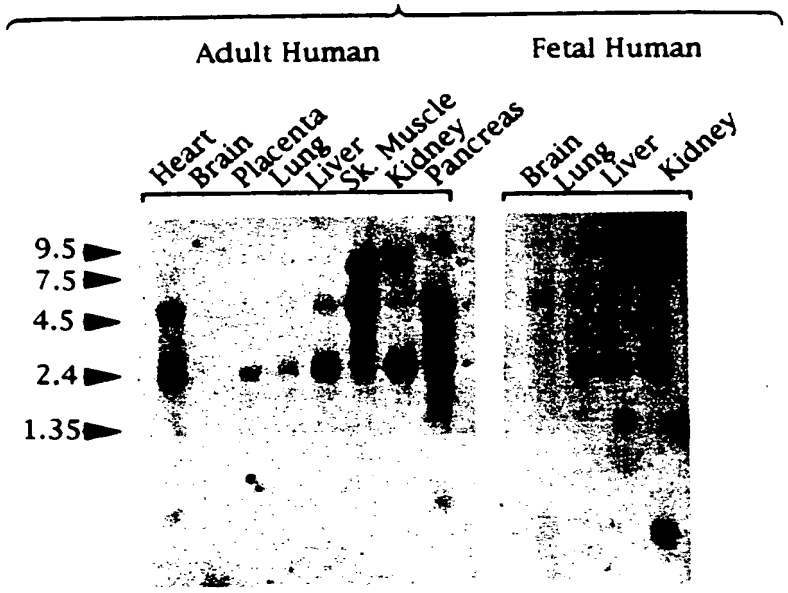

Adult Human
Fetal Human
Heart
Brain
Placenta
Lung
Liver
Sk. Muscle
Kidney
Pancreas
Brain
Lung
Liver
Kidney
9.5
7.5
4.5
2.4
1.35

FIG.4B

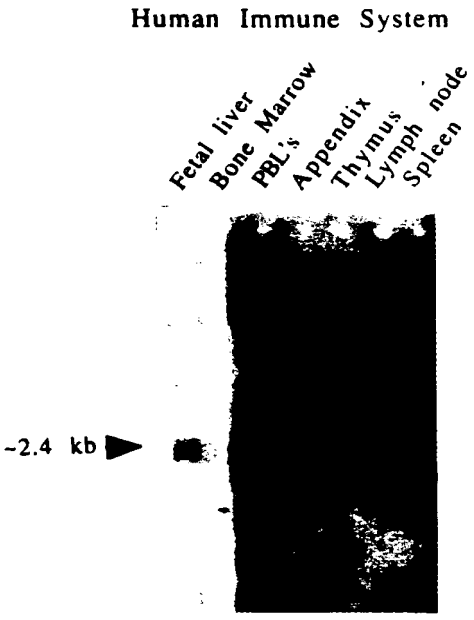
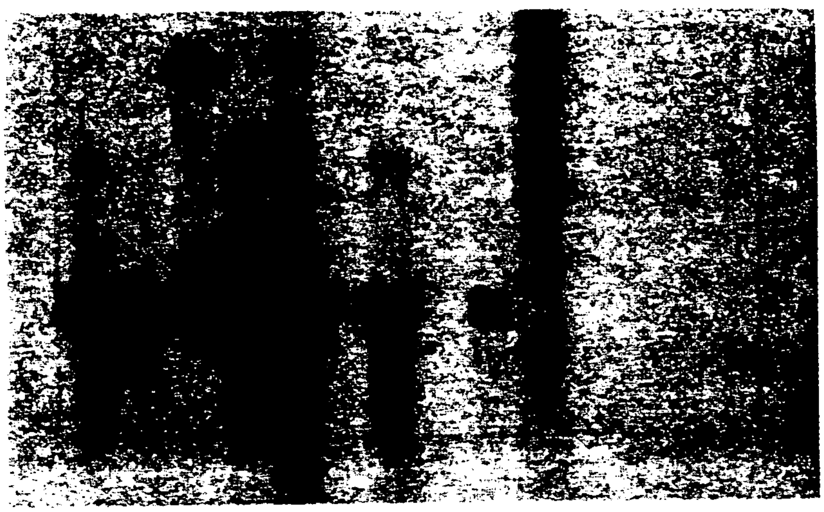

Human Immune System
Fetal liver
Bone Marrow
PBL's
Appendix
Thymus
Lymph node
Spleen
~2.4 kb

FIG.5



2 11 16 17 22 28 33 38 45 Kb 1 12 18 30

Transgenic Founders Controls

FIG.6A

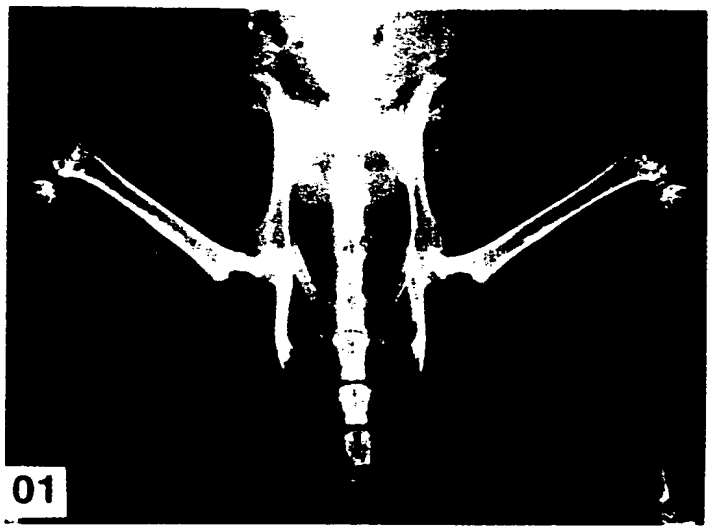


FIG.6B

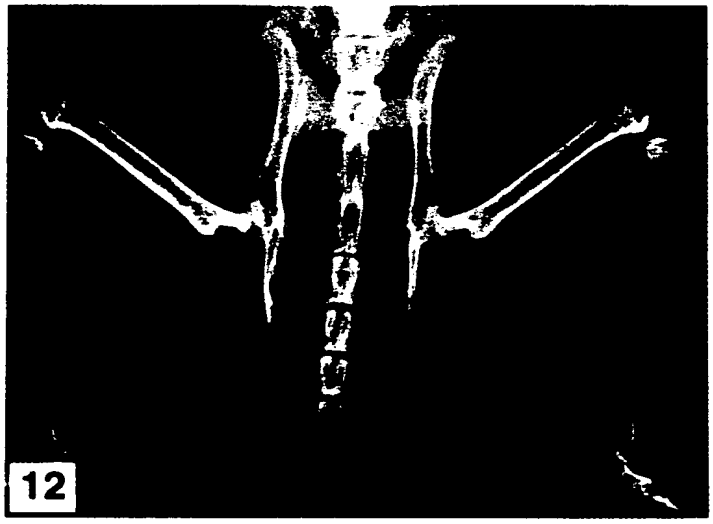


FIG.6C

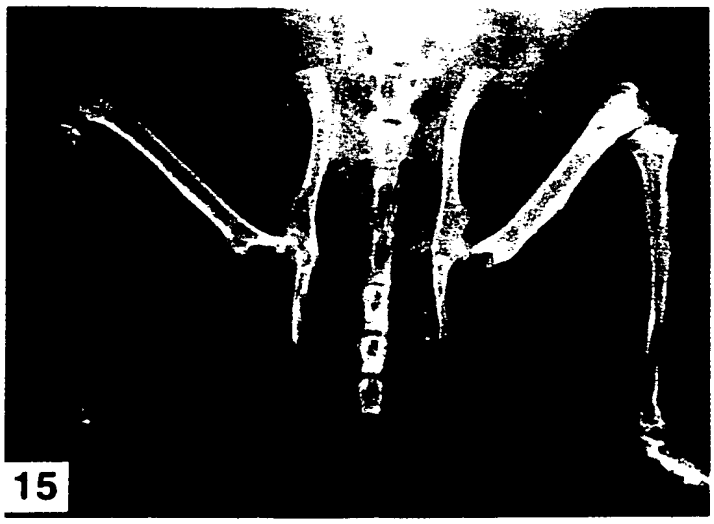


FIG.6D

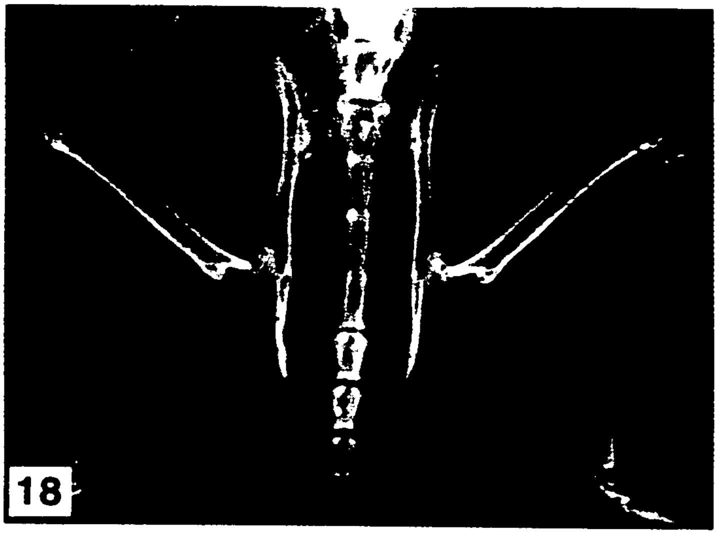


FIG.6E

FIG.6F

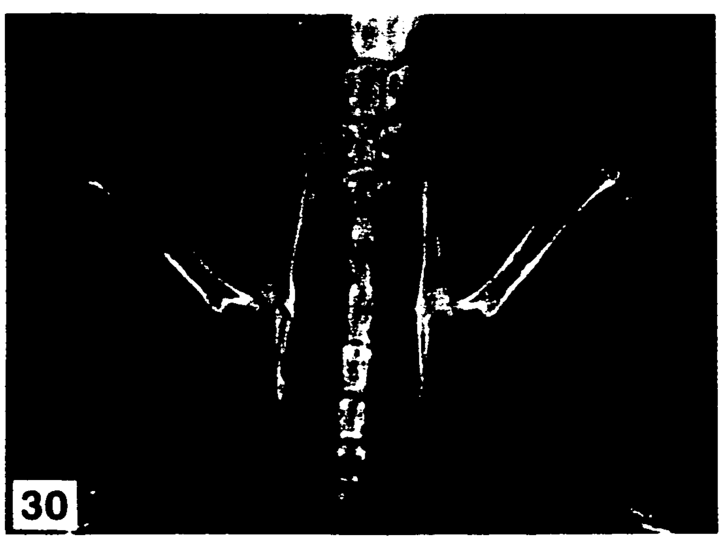


FIG.6G

FIG.6H

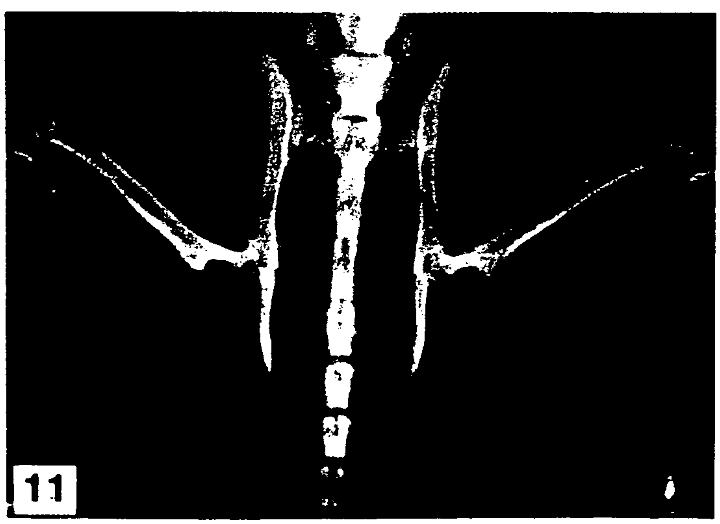


FIG.6I

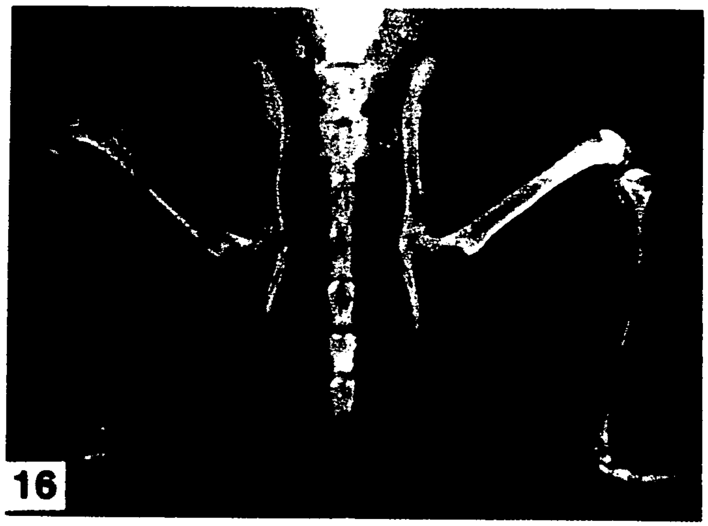


FIG.6J

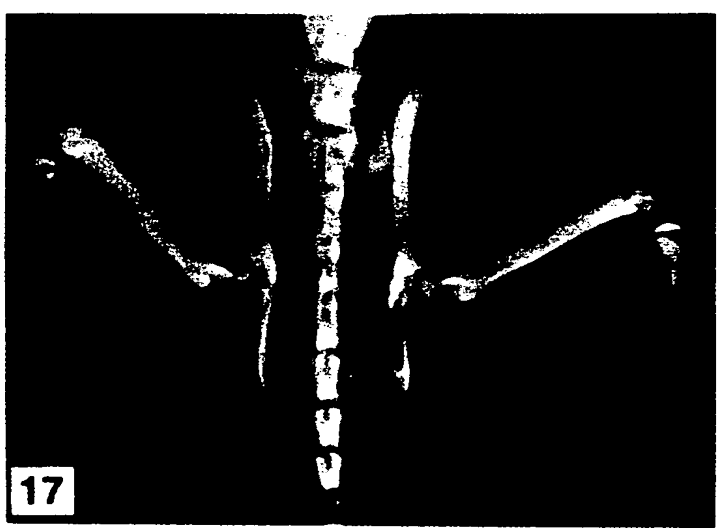


FIG.7A

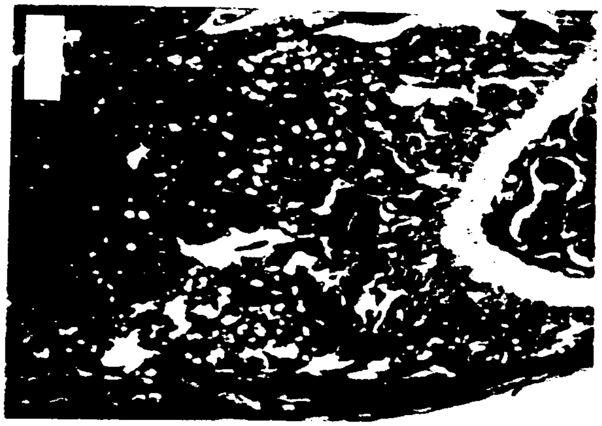


FIG.7B

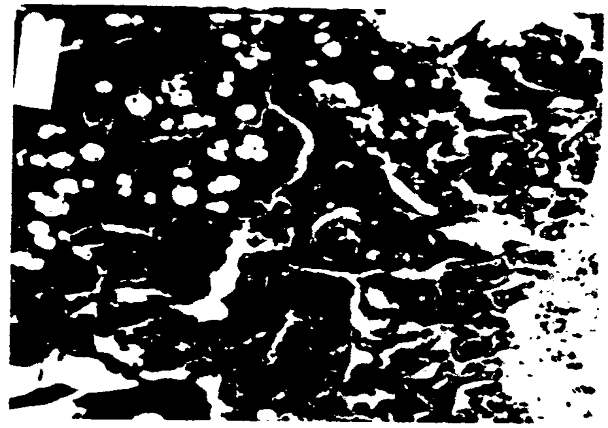


FIG.7C

FIG.7D

FIG.7E

FIG.7F

FIG.7G

FIG.7H

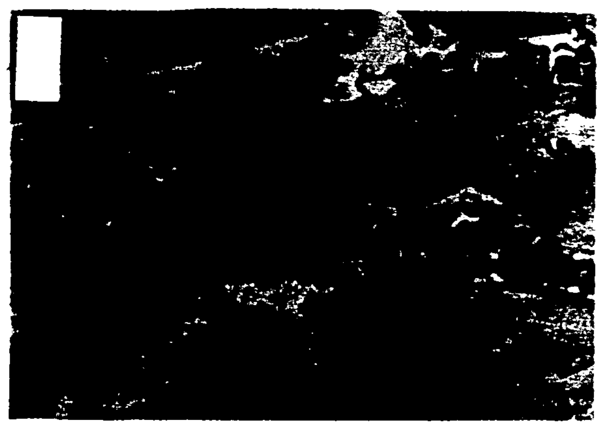


FIG.8A

FIG.8B

FIG.8C

FIG.8D

FIG.9A

10 30 50
CCTTATATAARACGTCATGATTGCCTGGGCTGCAGAGACGCACCTAGCACTGACCCAGCG
70 90 110
GCTGCCTCCTGAGGTTTCCCGAGGACCACAATGAACAAGTGGCTGTGCTGCGCACTCCTG
M N K W L C C A L L
130 150 170
GTGCTCCTGGACATCATTGAATGGACAACCCAGGAAACCCTTCCTCCAAAGTACTTGCAT
V L L D I I E W T T Q E T L P P K Y L H
190 210 230
TATGACCCAGAAACTGGTCATCAGCTCCTGTGTGACAAATGTGCTCCTGGCACCTACCTA
Y D P E T G H Q L L C D K C A P G T Y L
250 270 290
AAACAGCACTGCACAGTGAGGAGGAAGACATTGTGTGTCCCTTGCCCTGACCACTCTTAT
K Q H C T V R R K T L C V P C P D H S Y
310 330 350
ACGGACAGCTGGCACACCAGTGATGAGTGTGTGTATTGCAGCCCAGTGTGCAAGGAACTG
T D S W H T S D E C V Y C S P V C K E L
370 390 410
CAGTCCGTGAAGCAGGAGTGCAACCGCACCCACAACCGAGTGTGTGAGTGTGAGGAAGGG
Q S V K Q E C **N** R T H N R V C E C E E G
430 450 470
CGTTACCTGGAGATCGAATTCTGCTTGAAGCACCGGAGCTGTCCCCCGGGCTCCGGCGTG
R Y L E I E F C L K H R S C P P G S G V
490 510 530
GTGCAAGCTGGAACCCCAGAGCGAAACACAGTTTGCAAAAAATGTCCAGATGGGTTCTTC
V Q A G T P E R N T V C K K C P D G F F
550 570 590
TCAGGTGAGACTTCATCGAAAGCACCCTGTATAAAACACACGAACTGCAGCACATTTGGC
S G E T S S K A P C I K H T **N** C S T F G
610 630 650
CTCCTGCTAATTCAGAAAGGAAATGCAACACATGACAACGTGTGTTCCGGAAACAGAGAA
L L L I Q K G **N** A T H D N V C S G N R E
670 690 710
GCCACGCAAAAGTGTGGAATAGATGTCACCCTGTGTGAAGAGGCCTTCTTCAGGTTTGCT
A T Q K C G I D V T L C E E A F F R F A
730 750 770
GTTCCTACCAAGATTATACCAAATTGGCTGAGTGTTTTGGTGGACAGTTTGCCTGGGACC
V P T K I I P N W L S V L V D S L P G T

FIG.9B

```
        790                   810                   830
AAAGTGAATGCCGAGAGTGTAGAGAGGATAAAACGGAGACACAGCTCACAAGAGCAAACC
K  V  N  A  E  S  V  E  R  I  K  R  R  H  S  S  Q  E  Q  T
        850                   870                   890
TTCCAGCTGCTGAAGCTGTGGAAACATCAAAACAGAGACCAGGAAATGGTGAAGAAGATC
F  Q  L  L  K  L  W  K  H  Q  N  R  D  Q  E  M  V  K  K  I
        910                   930                   950
ATCCAAGACATTGACCTCTGTGAAAGCAGCGTGCAGCGGCATCTCGGCCACTCGAACCTC
I  Q  D  I  D  L  C  E  S  S  V  Q  R  H  L  G  H  S  N  L
        970                   990                  1010
ACCACAGAGCAGCTTCTTGCCTTGATGGAGAGCCTGCCTGGGAAGAAGATCAGCCCAGAA
T  T  E  Q  L  L  A  L  M  E  S  L  P  G  K  K  I  S  P  E
       1030                  1050                  1070
GAGATTGAGAGAACGAGAAAGACCTGCAAATCGAGCGAGCAGCTCCTGAAGCTACTCAGT
E  I  E  R  T  R  K  T  C  K  S  S  E  Q  L  L  K  L  L  S
       1090                  1110                  1130
TTATGGAGGATCAAAAATGGTGACCAAGACACCTTGAAGGGCCTGATGTATGCCCTCAAG
L  W  R  I  K  N  G  D  Q  D  T  L  K  G  L  M  Y  A  L  K
       1150                  1170                  1190
CACTTGAAAACATCCCACTTTCCCAAAACTGTCACCCACAGTCTGAGGAAGACCATGAGG
H  L  K  T  S  H  F  P  K  T  V  T  H  S  L  R  K  T  M  R
       1210                  1230                  1250
TTCCTGCACAGCTTCACAATGTACAGACTGTATCAGAAGCTCTTTTTAGAAATGATAGGG
F  L  H  S  F  T  M  Y  R  L  Y  Q  K  L  F  L  E  M  I  G
       1270                  1290                  1310
AATCAGGTTCAATCCGTGAAAATAAGCTGCTTATAACTAGGAATGGTCACTGGGCTGTTT
N  Q  V  Q  S  V  K  I  S  C  L

CTTCA
```

FIG.9C

```
         10                       30                        50
GTATATATAACGTGATGAGCGTACGGGTGCGGAGACGCACCGGAGCGCTCGCCCAGCCGC
         70                       90                       110
CGYCTCCAAGCCCCTGAGGTTTCCGGGGACCACAATGAACAAGTTGCTGTGCTGCGCGCT
                                     M  N  K  L  L  C  C  A  L
        130                      150                       170
CGTGTTTCTGGACATCTCCATTAAGTGGACCACCCAGGAAACGTTTCCTCCAAAGTACCT
 V  F  L  D  I  S  I  K  W  T  T  Q  E  T  F  P  P  K  Y  L
        190                      210                       230
TCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCTCCTGGTACCTA
 H  Y  D  E  E  T  S  H  Q  L  L  C  D  K  C  P  P  G  T  Y
        250                      270                       290
CCTAAAACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCTTGCCCTGACCACTA
 L  K  Q  H  C  T  A  K  W  K  T  V  C  A  P  C  P  D  H  Y
        310                      330                       350
CTACACAGACAGCTGGCACACCAGTGACGAGTGTCTATACTGCAGCCCCGTGTGCAAGGA
 Y  T  D  S  W  H  T  S  D  E  C  L  Y  C  S  P  V  C  K  E
        370                      390                       410
GCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGCGAATGCAAGGA
 L  Q  Y  V  K  Q  E  C  N  R  T  H  N  R  V  C  E  C  K  E
        430                      450                       470
AGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGCTGCCCTCCTGGATTTGG
 G  R  Y  L  E  I  E  F  C  L  K  H  R  S  C  P  P  G  F  G
        490                      510                       530
AGTGGTGCAAGCTGGAACCCCAGAGCGAAATACAGTTTGCAAAAGATGTCCAGATGGGTT
 V  V  Q  A  G  T  P  E  R  N  T  V  C  K  R  C  P  D  G  F
        550                      570                       590
CTTCTCAAATGAGACGTCATCTAAAGCACCCTGTAGAAAACACACAAATTGCAGTGTCTT
 F  S  N  E  T  S  S  K  A  P  C  R  K  H  T  N  C  S  V  F
        610                      630                       650
TGGTCTCCTGCTAACTCAGAAAGGAAATGCAACACACGACAACATATGTTCCGGAAACAG
 G  L  L  L  T  Q  K  G  N  A  T  H  D  N  I  C  S  G  N  S
        670                      690                       710
TGAATCAACTCAAAAATGTGGAATAGATGTTACCCTGTGTGAGGAGGCATTCTTCAGGTT
 E  S  T  Q  K  C  G  I  D  V  T  L  C  E  E  A  F  F  R  F
        730                      750                       770
TGCTGTTCCTACAAAGTTTACGCCTAACTGGCTTAGTGTCTTGGTAGACAATTTGCCTGG
 A  V  P  T  K  F  T  P  N  W  L  S  V  L  V  D  N  L  P  G
```

FIG.9D

```
        790                       810                       830
CACCAAAGTAAACGCAGAGAGTGTAGAGAGGATAAAACGGCAACACAGCTCACAAGAACA
 T  K  V  N  A  E  S  V  E  R  I  K  R  Q  H  S  S  Q  E  Q
        850                       870                       890
GACTTTCCAGCTGCTGAAGTTATGGAAACATCAAAACAAAGACCAAGATATAGTCAAGAA
 T  F  Q  L  L  K  L  W  K  H  Q  N  K  D  Q  D  I  V  K  K
        910                       930                       950
GATCATCCAAGATATTGACCTCTGTGAAAACAGCGTGCAGCGGCACATTGGACATGCTAA
 I  I  Q  D  I  D  L  C  E  N  S  V  Q  R  H  I  G  H  A  N
        970                       990                      1010
CCTCACCTTCGAGCAGCTTCGTAGCTTGATGGAAAGCTTACCGGGAAAGAAAGTGGGAGC
 L  T  F  E  Q  L  R  S  L  M  E  S  L  P  G  K  K  V  G  A
       1030                      1050                      1070
AGAAGACATTGAAAAAACAATAAAGGCATGCAAACCCAGTGACCAGATCCTGAAGCTGCT
 E  D  I  E  K  T  I  K  A  C  K  P  S  D  Q  I  L  K  L  L
       1090                      1110                      1130
CAGTTTGTGGCGAATAAAAAATGGCGACCAAGACACCTTGAAGGGCCTAATGCACGCACT
 S  L  W  R  I  K  N  G  D  Q  D  T  L  K  G  L  M  H  A  L
       1150                      1170                      1190
AAAGCACTCAAAGACGTACCACTTTCCCAAAACTGTCACTCAGAGTCTAAAGAAGACCAT
 K  H  S  K  T  Y  H  F  P  K  T  V  T  Q  S  L  K  K  T  I
       1210                      1230                      1250
CAGGTTCCTTCACAGCTTCACAATGTACAAATTGTATCAGAAGTTATTTTTAGAAATGAT
 R  F  L  H  S  F  T  M  Y  K  L  Y  Q  K  L  F  L  E  M  I
       1270                      1290                      1310
AGGTAACCAGGTCCAATCAGTAAAAATAAGCTGCTTATAACTGGAAATGGCCATTGAGCT
 G  N  Q  V  Q  S  V  K  I  S  C  L
       1330                      1350
GTTTCCTCACAATTGGCGAGATCCCATGGATGATAA
```

FIG.9E

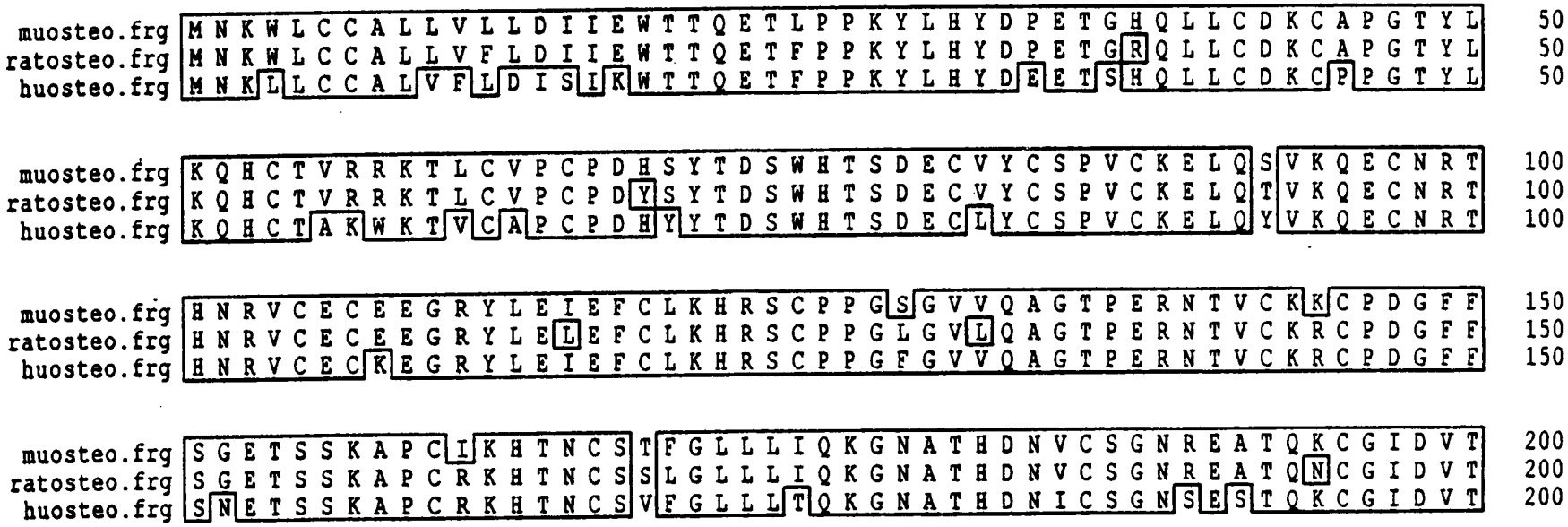


FIG.9F

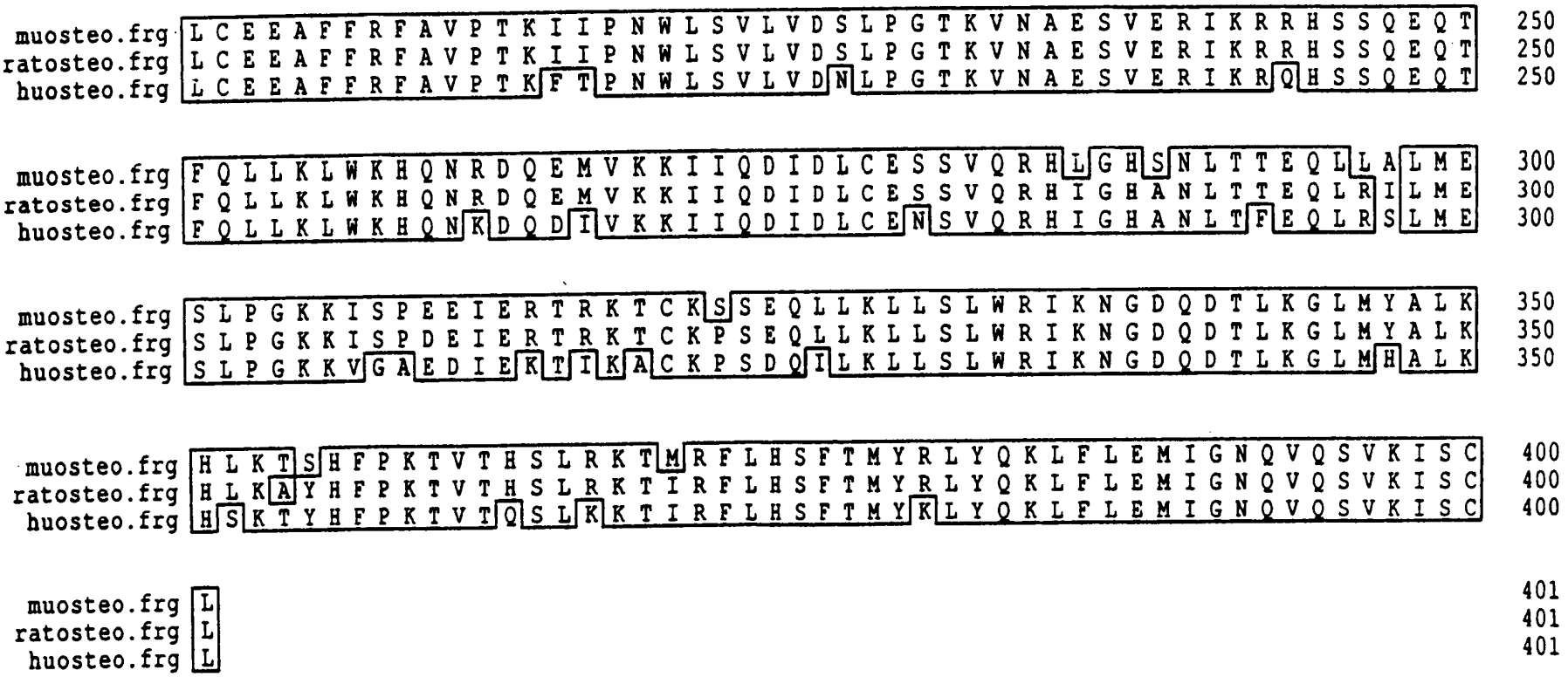

muosteo.frg L C E E A F F R F A V P T K I I P N W L S V L V D S L P G T K V N A E S V E R I K R R H S S Q E Q T 250
ratosteo.frg L C E E A F F R F A V P T K I I P N W L S V L V D S L P G T K V N A E S V E R I K R R H S S Q E Q T 250
huosteo.frg L C E E A F F R F A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R I K R Q H S S Q E Q T 250
muosteo.frg F Q L L K L W K H Q N R D Q E M V K K I I Q D I D L C E S S V Q R H L G H S N L T T E Q L L A L M E 300
ratosteo.frg F Q L L K L W K H Q N R D Q E M V K K I I Q D I D L C E S S V Q R H I G H A N L T T E Q L R I L M E 300
huosteo.frg F Q L L K L W K H Q N K D Q D I V K K I I Q D I D L C E N S V Q R H I G H A N L T F E Q L R S L M E 300
muosteo.frg S L P G K K I S P E E I E R T R K T C K S S E Q L L K L L S L W R I K N G D Q D T L K G L M Y A L K 350
ratosteo.frg S L P G K K I S P D E I E R T R K T C K P S E Q L L K L L S L W R I K N G D Q D T L K G L M Y A L K 350
huosteo.frg S L P G K K V G A E D I E K T I K A C K P S D Q I L K L L S L W R I K N G D Q D T L K G L M H A L K 350
muosteo.frg H L K T S H F P K T V T H S L R K T M R F L H S F T M Y R L Y Q K L F L E M I G N Q V Q S V K I S C 400
ratosteo.frg H L K A Y H F P K T V T H S L R K T I R F L H S F T M Y R L Y Q K L F L E M I G N Q V Q S V K I S C 400
huosteo.frg H S K T Y H F P K T V T Q S L K K T I R F L H S F T M Y K L Y Q K L F L E M I G N Q V Q S V K I S C 400
muosteo.frg L 401
ratosteo.frg L 401
huosteo.frg L 401

FIG.10

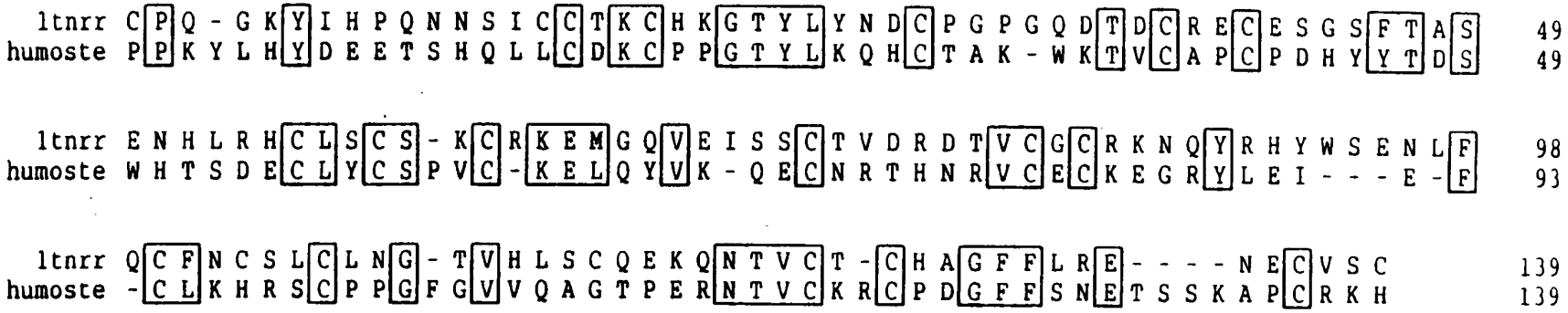


FIG. 11

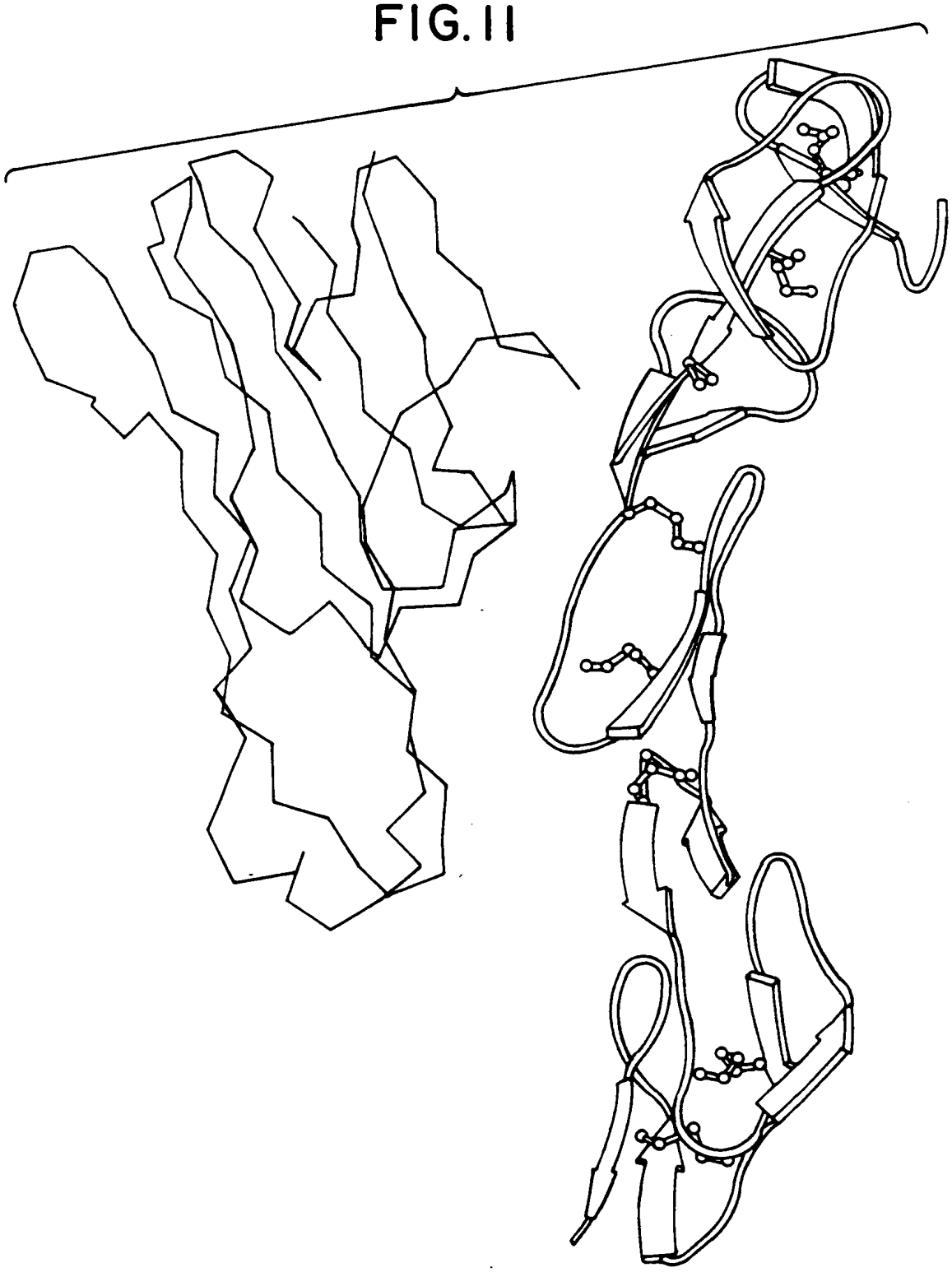


FIG.12A

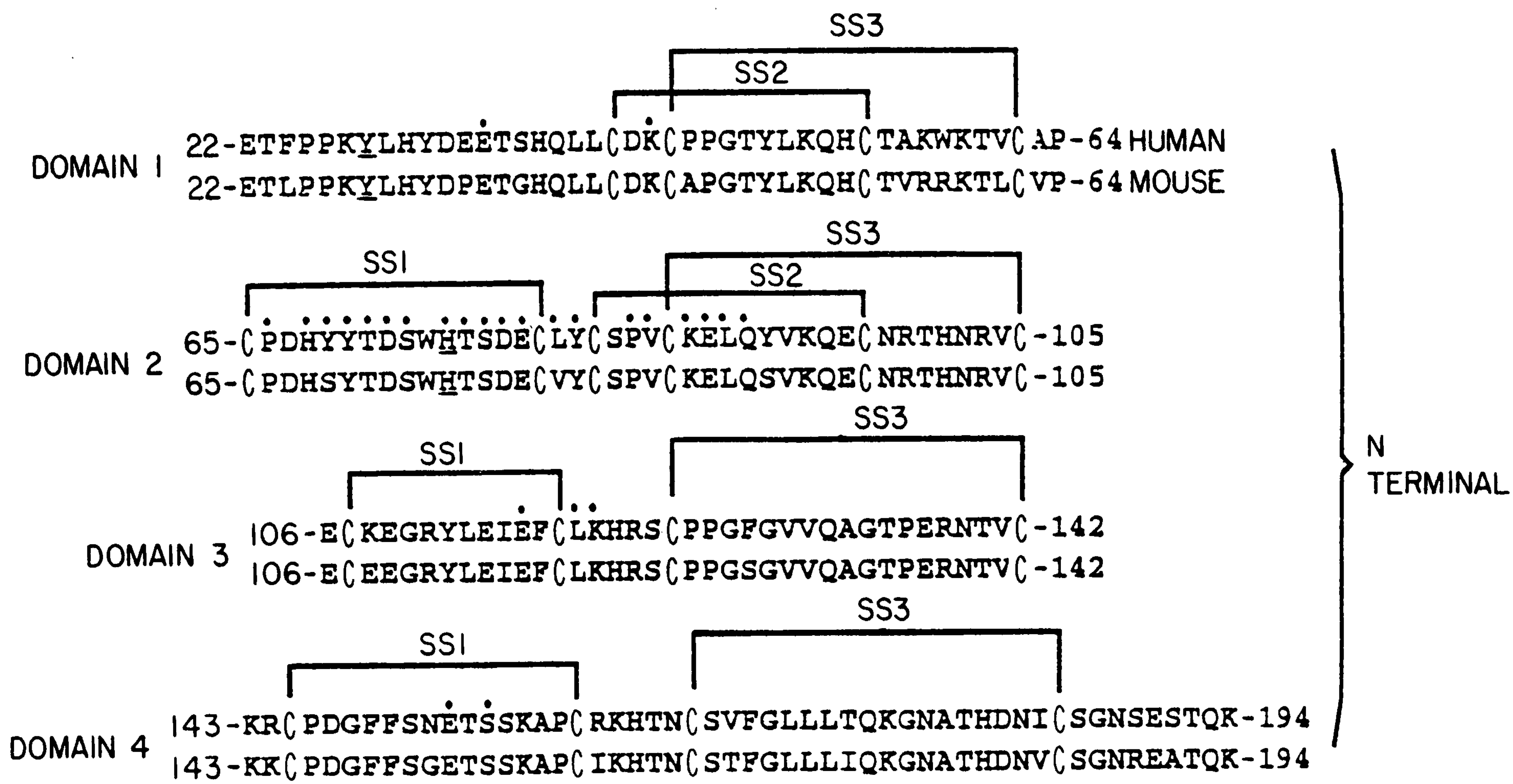

SS3
SS2
DOMAIN 1
22-ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAP-64 HUMAN
22-ETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVP-64 MOUSE
SSI
SS3
SS2
DOMAIN 2
65-CPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVC-105
65-CPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVC-105
SSI
SS3
DOMAIN 3
106-ECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVC-142
106-ECEEGRYLEIEFCLKHRSCPPGSGVVQAGTPERNTVC-142
SSI
SS3
DOMAIN 4
143-KRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQK-194
143-KKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVCSGNREATQK-194
N TERMINAL

FIG.12B

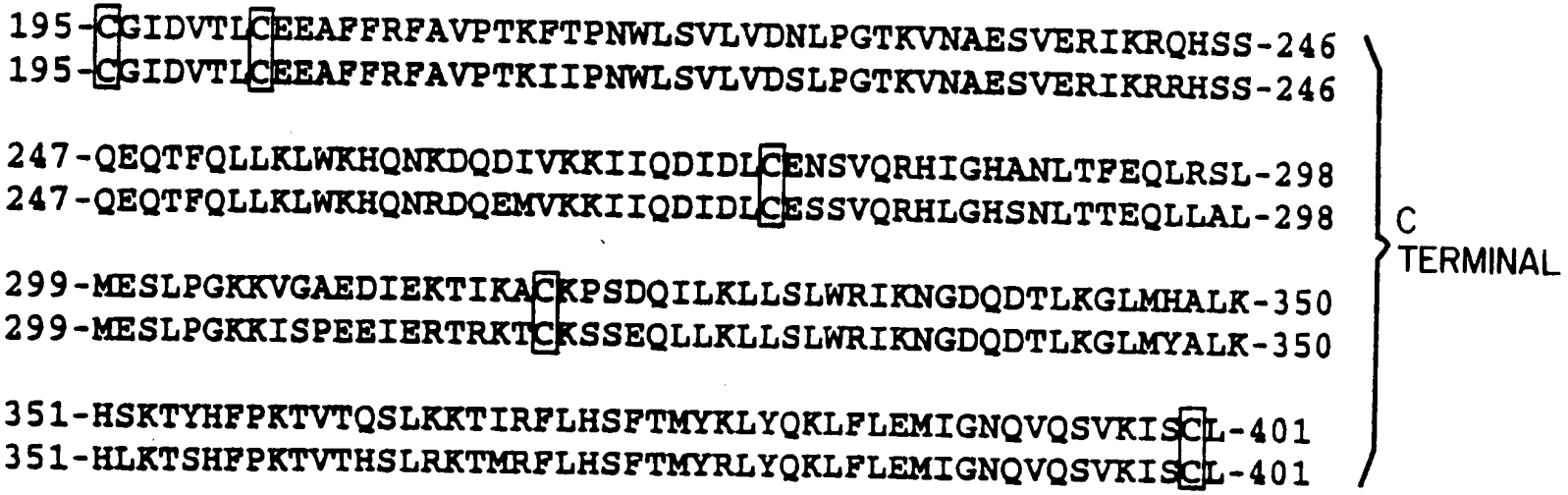


FIG.13A

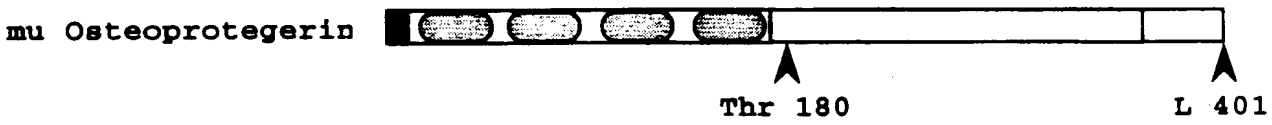


FIG.13B

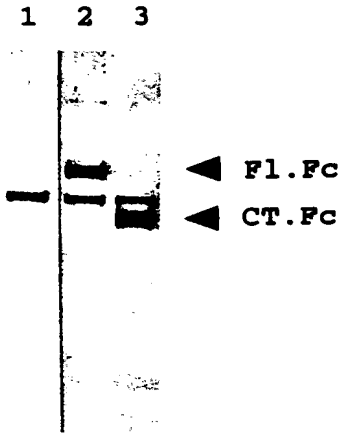


FIG.13C

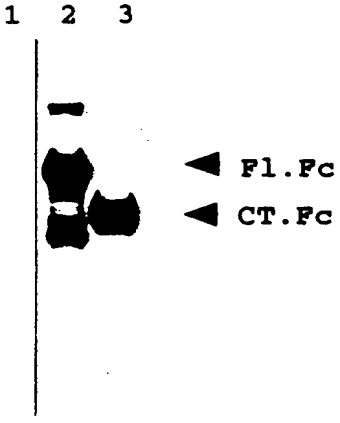


FIG.14A

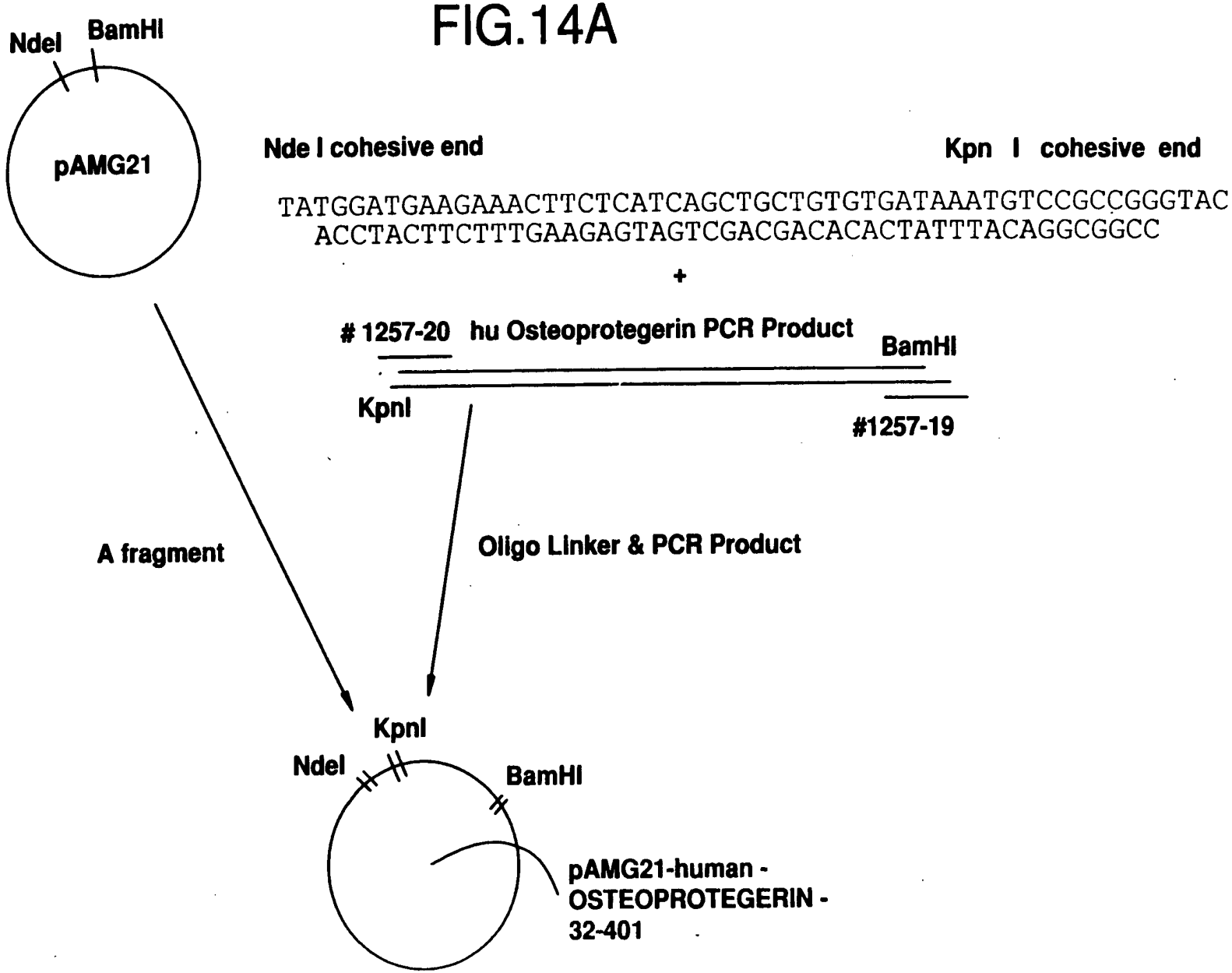


FIG.14B

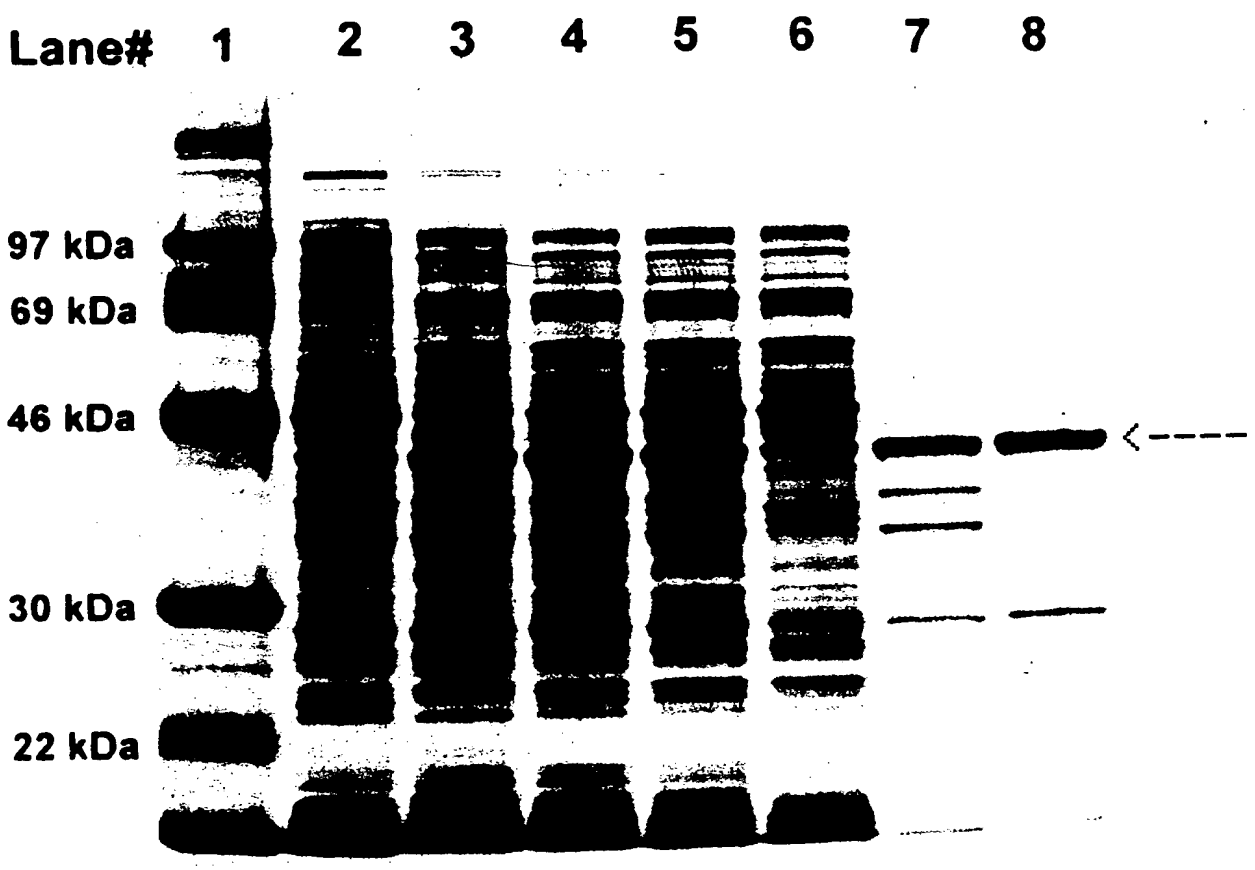


FIG. 15

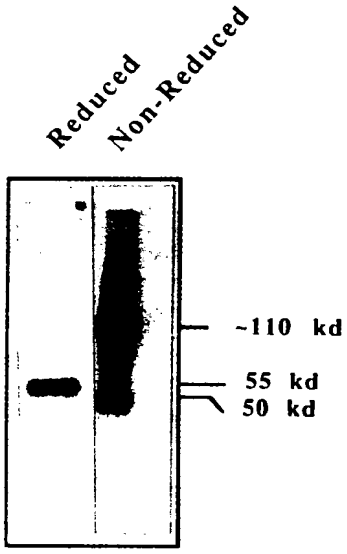


FIG.16A

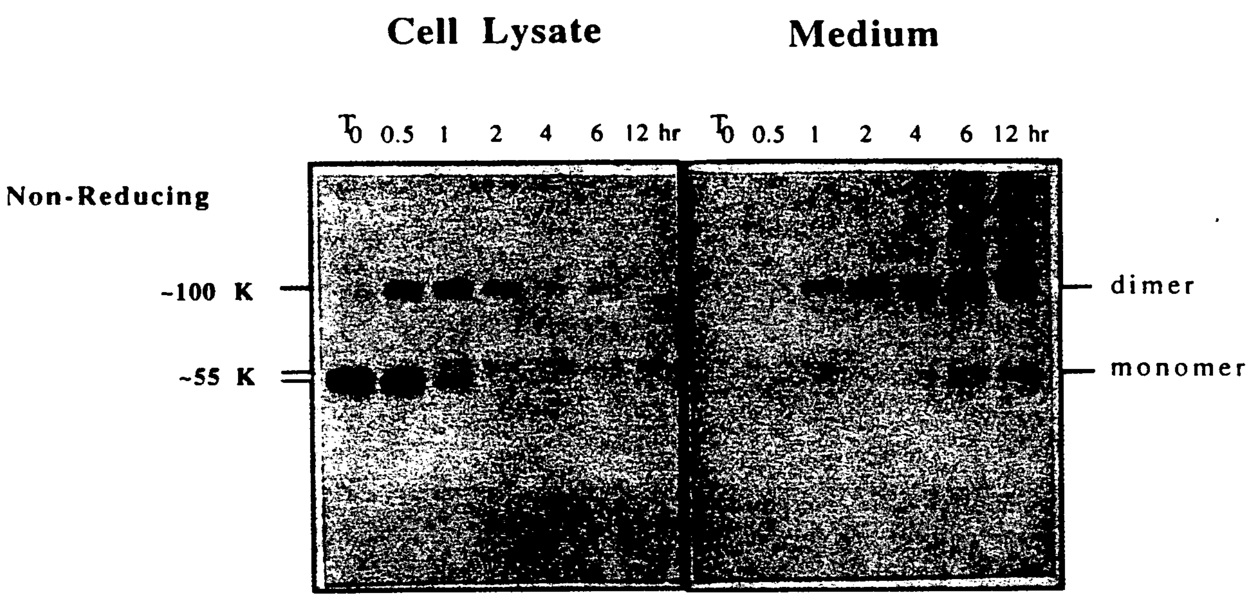


FIG.16B

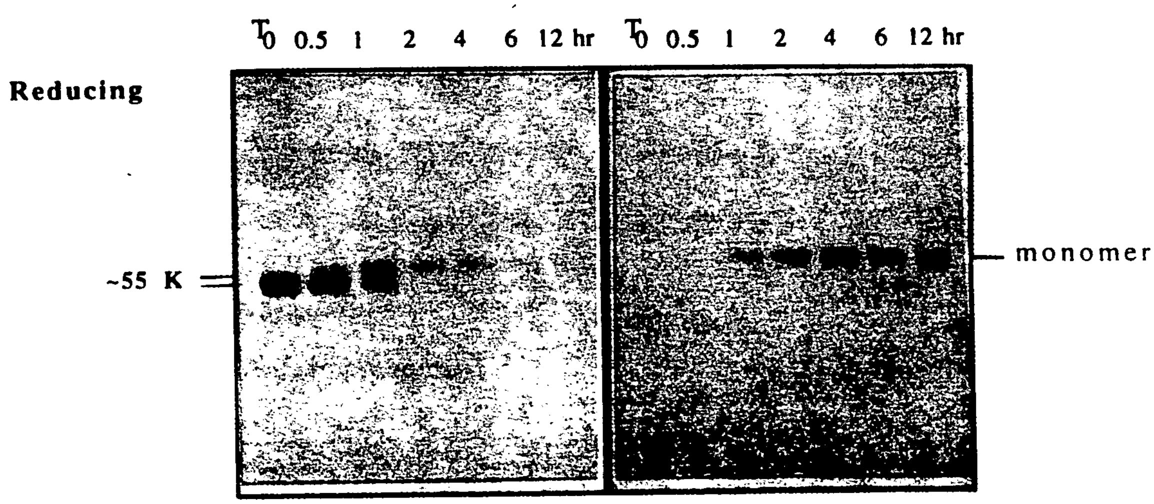


FIG.17

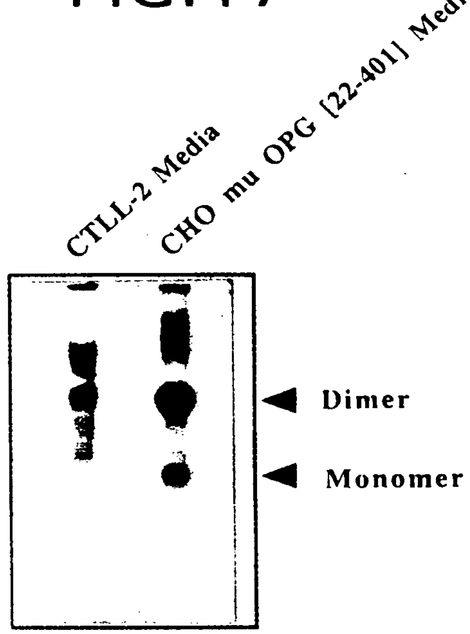


FIG.18

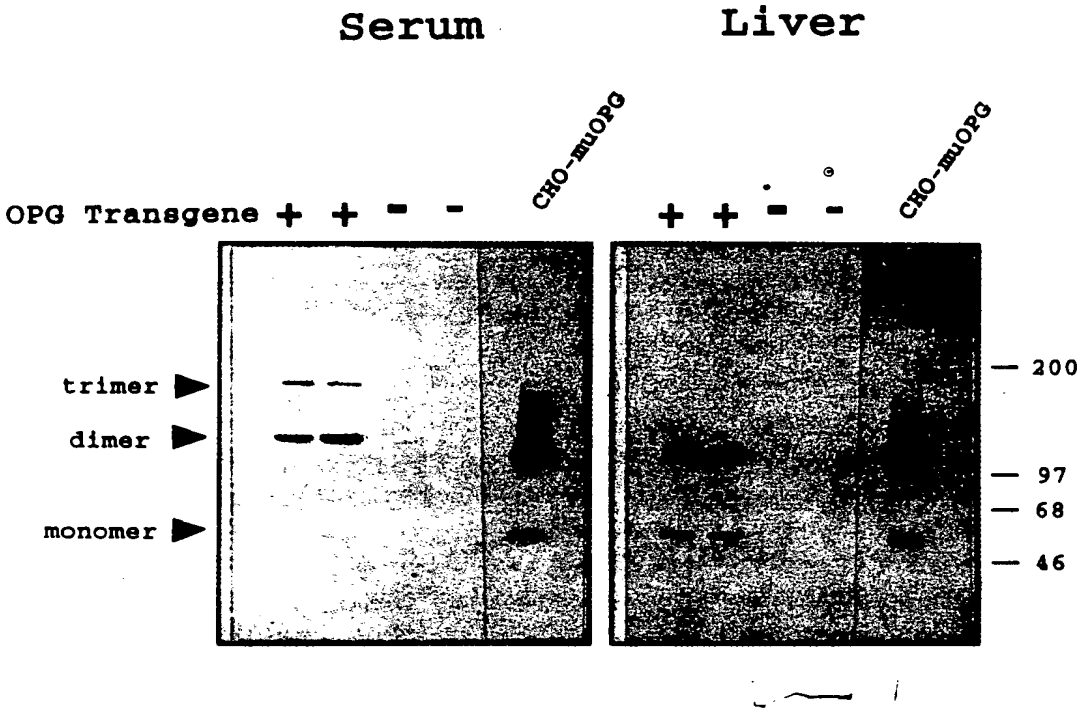

Serum
Liver
OPG Transgene + + - - CHO-muOPG
+ + - - CHO-muOPG
trimer
dimer
monomer
200
97
68
46

FIG.19A

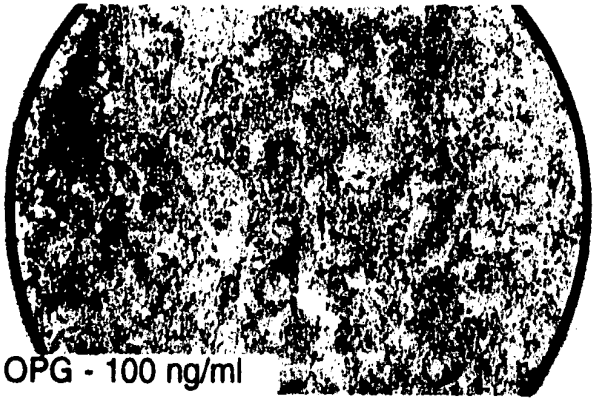


FIG.19B

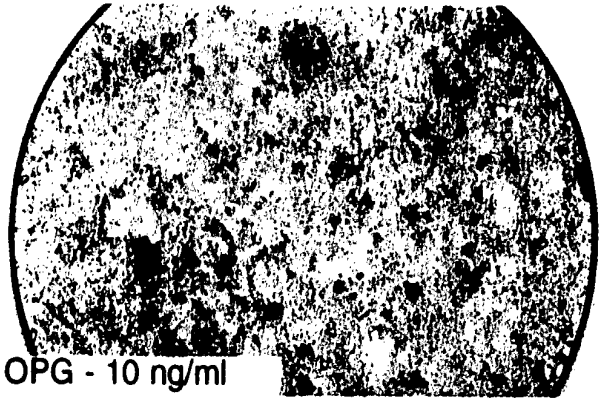


FIG.19C

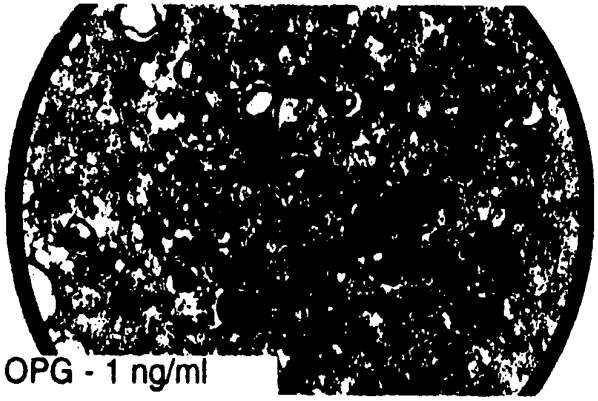


FIG.19D

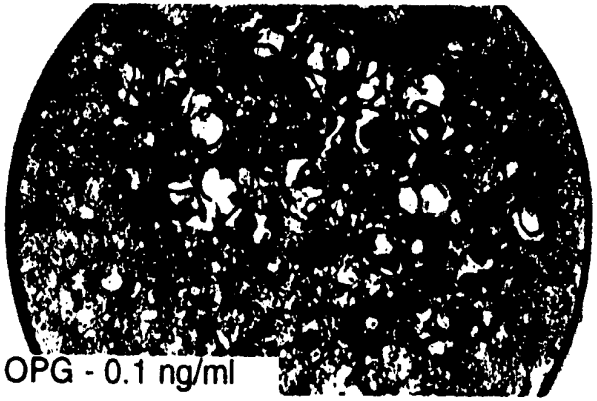


FIG.19E

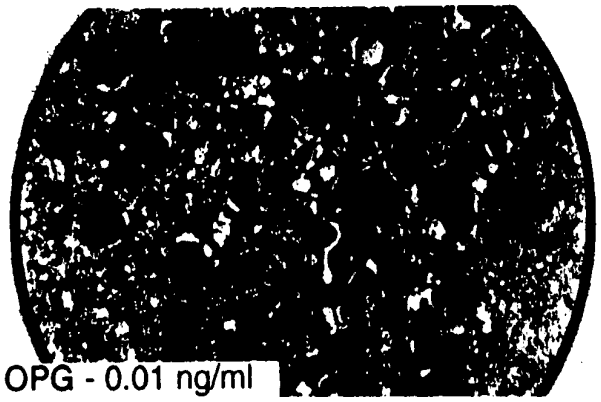


FIG.19F

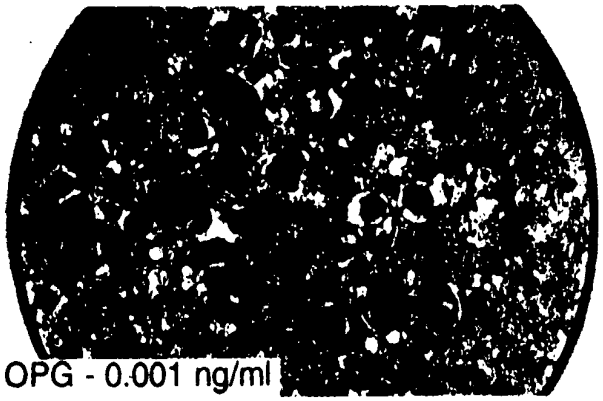


FIG.19G

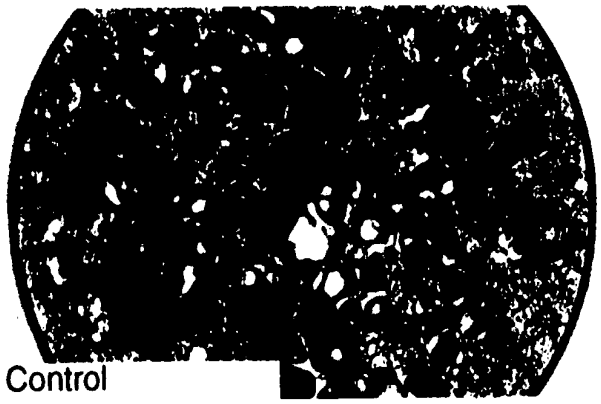


FIG.20

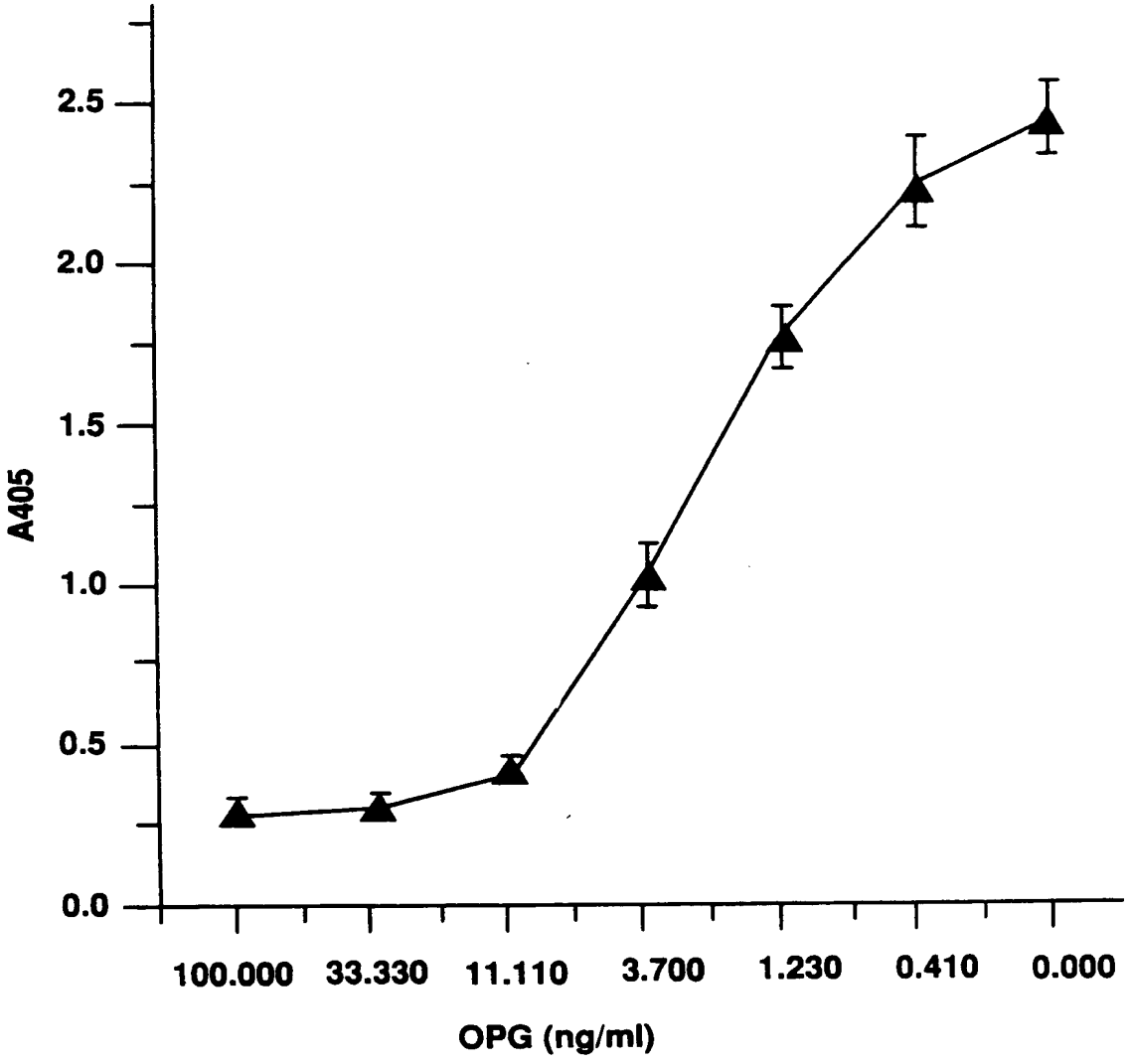
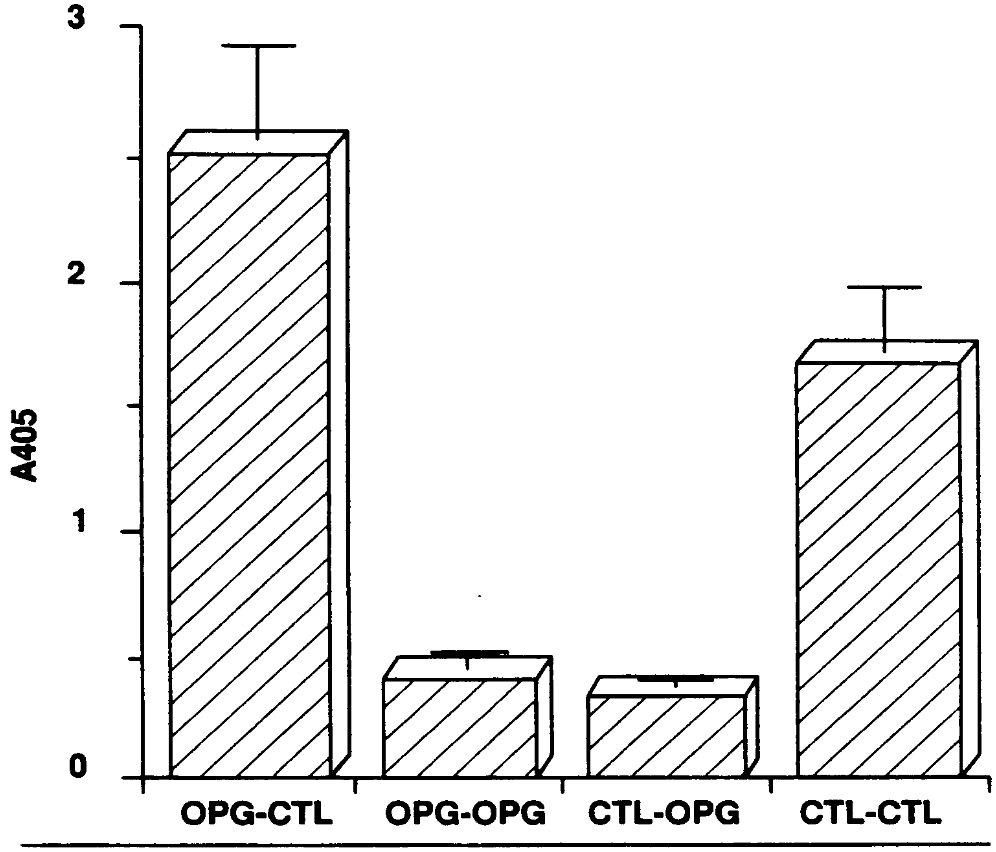

2.5
2.0
1.5
1.0
0.5
0.0
A405
100.000
33.330
11.110
3.700
1.230
0.410
0.000
OPG (ng/ml)

FIG.21



Legend

Growth	Intermediate	Terminal
Bone marrow cells CSF -1	PGE2 + CSF-1	ST2 cells 1,25 (OH)2 D3 Dexamethasone
4 days	2 days	8 - 10 days

Groups	OPG	OPG
CTL - CTL	— — —	— — —
OPG - CTL	100 ng/ml	— — —
OPG - OPG	— — —	100 ng/ml
OPG - OPG	100 ng/ml	100 ng/ml

FIG.22A

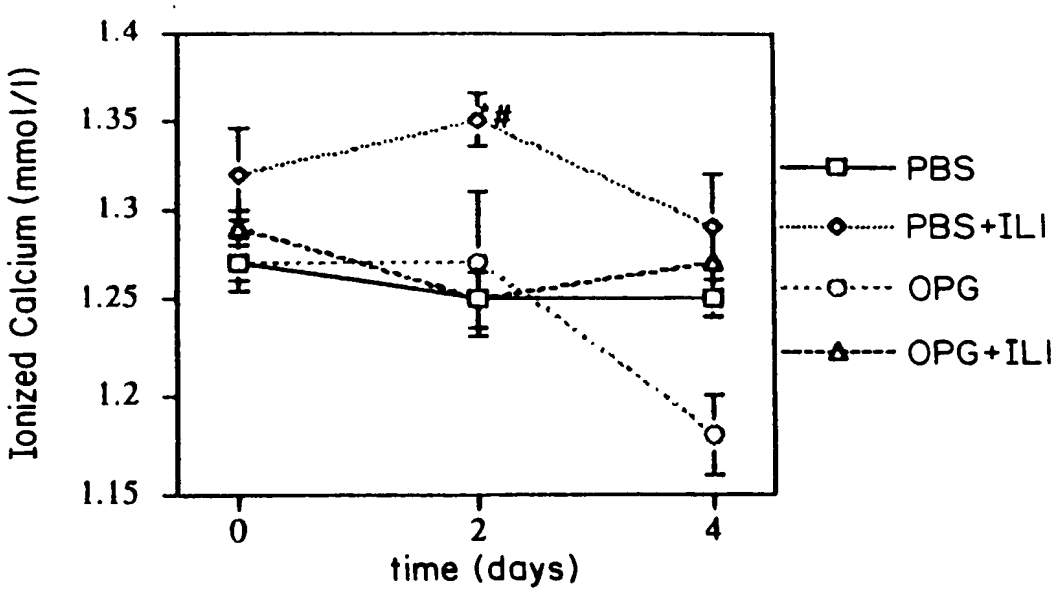
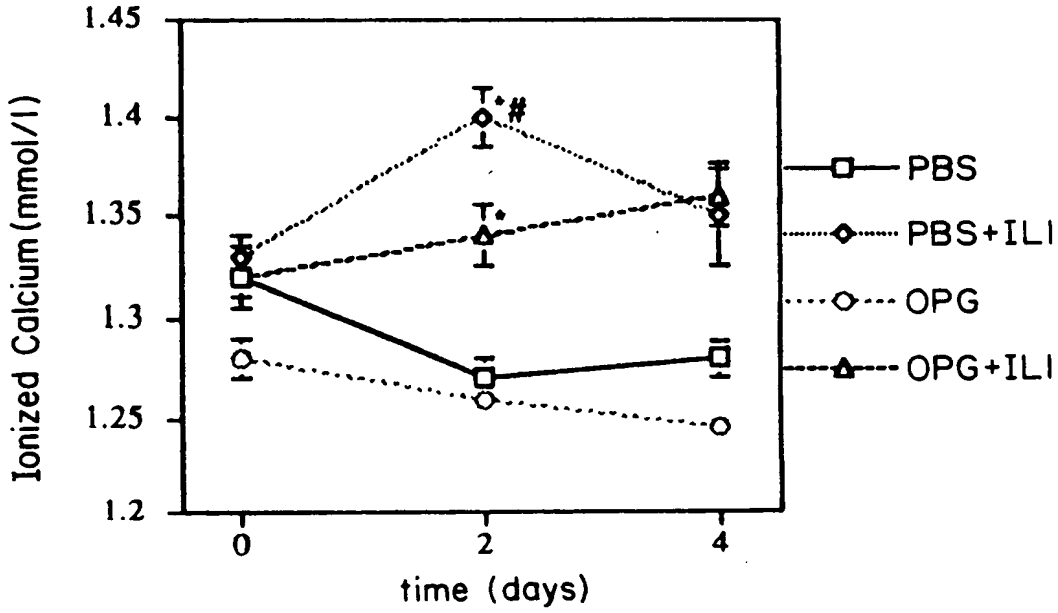


FIG.22B



* Different to PBS, $p < 0.05$
# Different to OPG + IL1, $p < 0.05$

FIG.23A

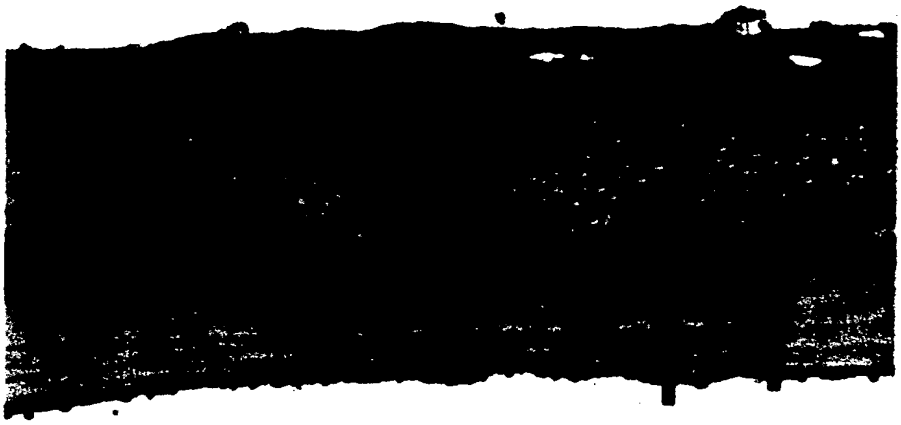


FIG.23B

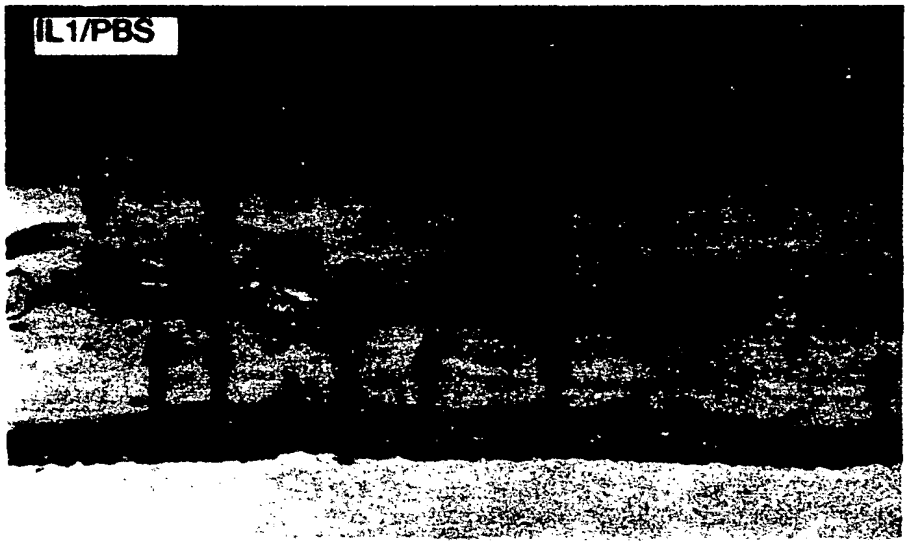


FIG.23C

PBS/OPG

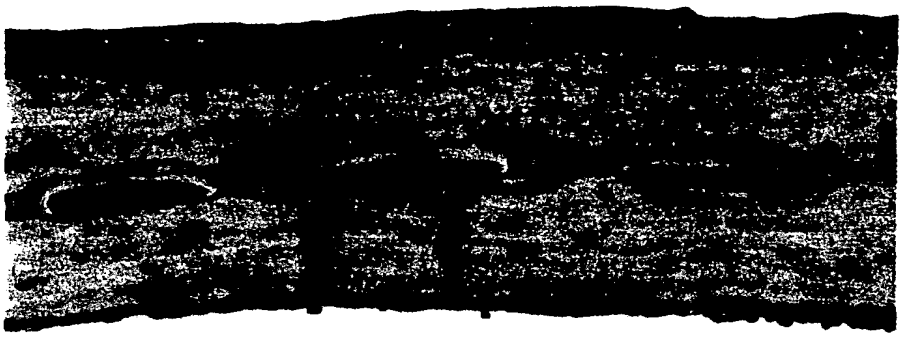
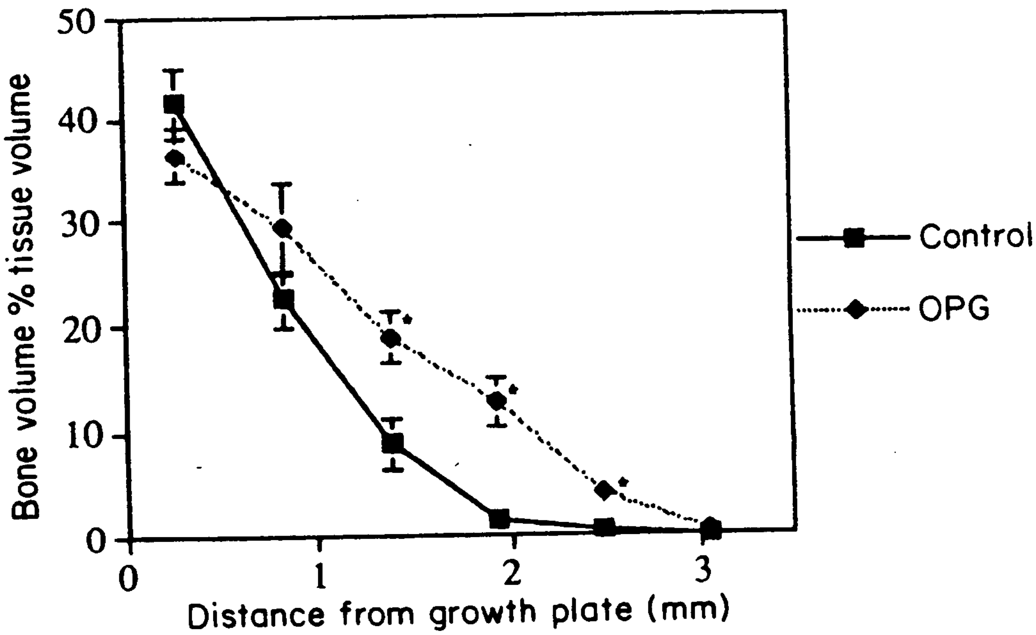


FIG.23D

FIG.24A

FIG.24B

FIG.25



* Different to control $p < 0.01$

FIG.26A FIG.26.B

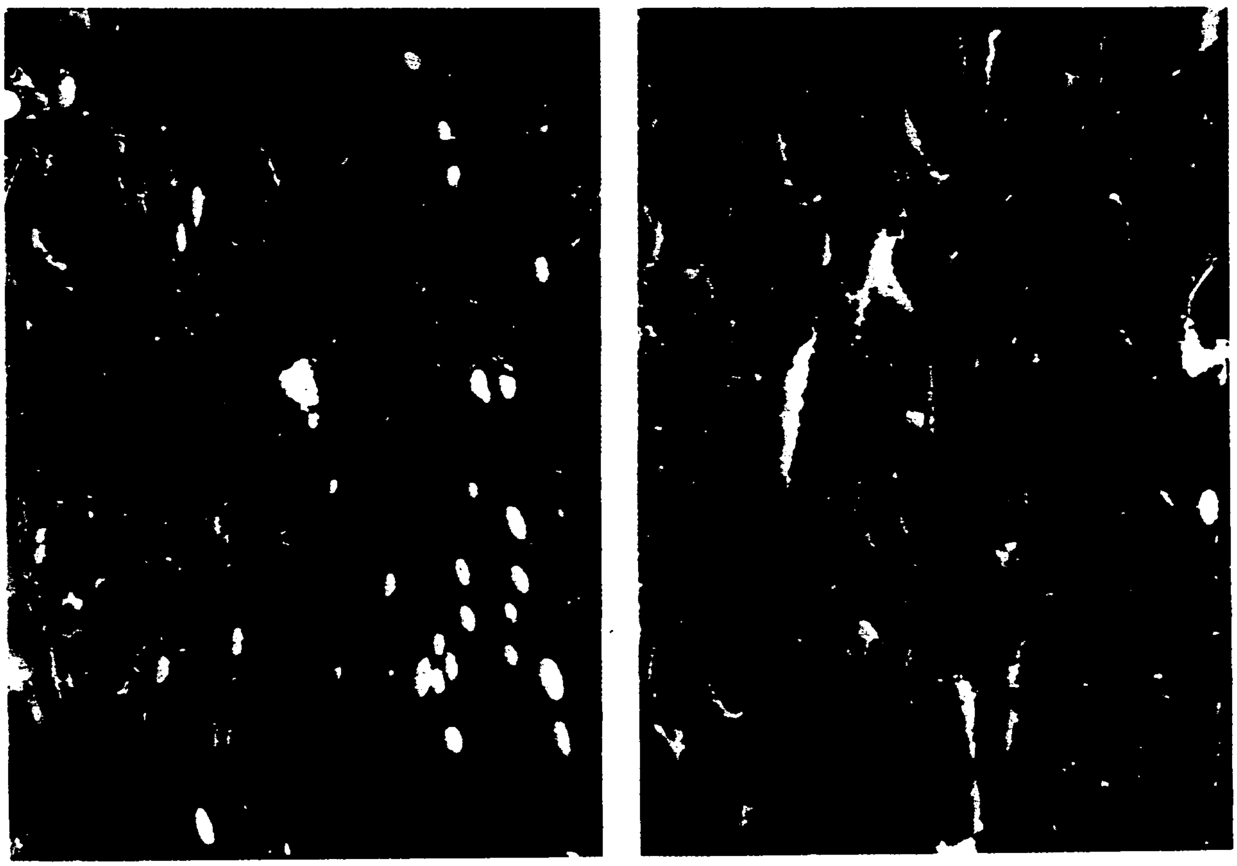


FIG.27

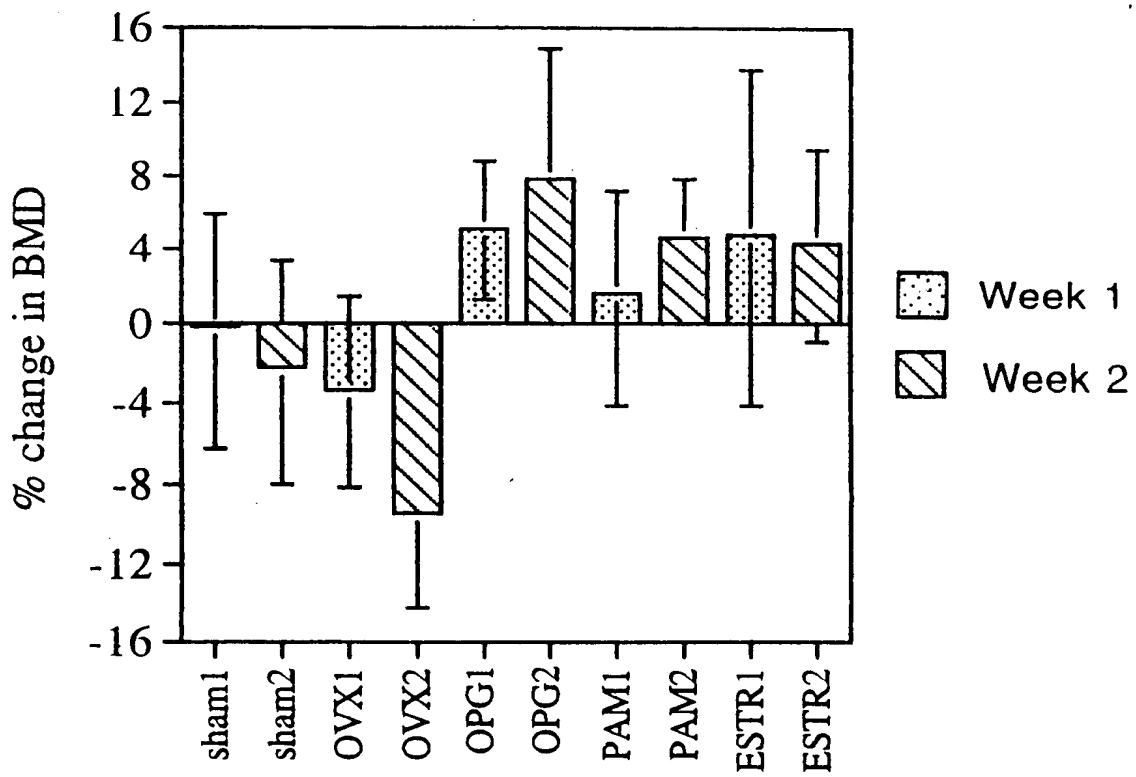
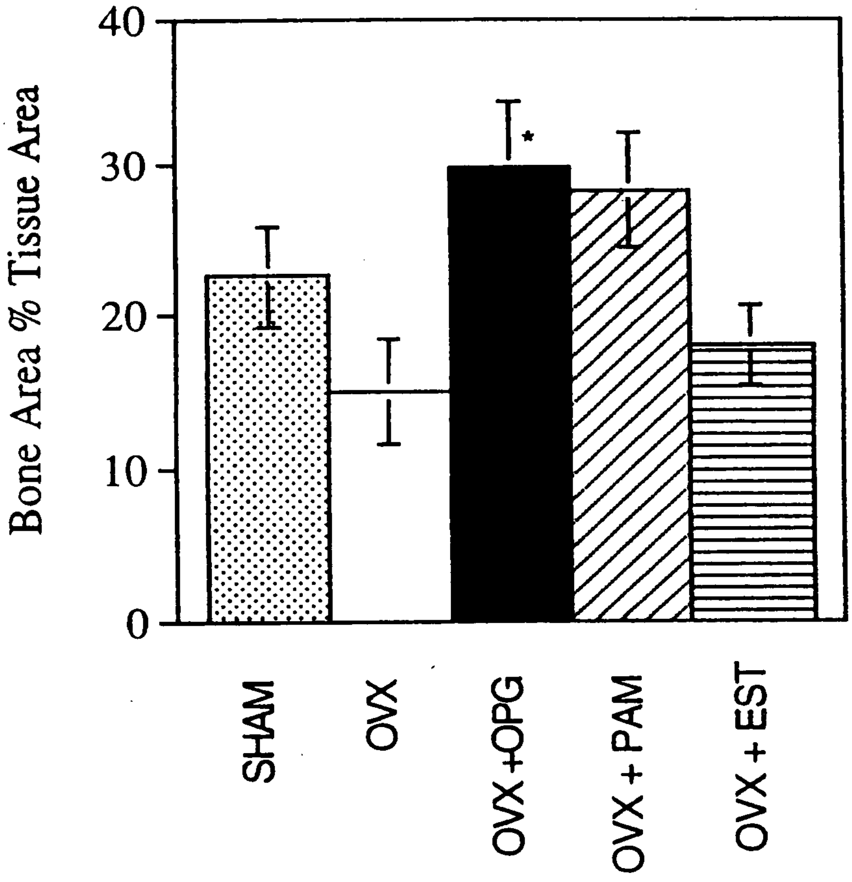

16
12
8
4
0
-4
-8
-12
-16
% change in BMD
sham1
sham2
OVX1
OVX2
OPG1
OPG2
PAM1
PAM2
ESTR1
ESTR2
Week 1
Week 2

FIG.28



* Different to OVX $p < 0.05$